

SEQUENCE LISTING

<110> Scalato, Enzo
Masignani, Vega
Rappuoli, Rino
Pizza, Mariagrazia
Grandi, Guido

<120> Meningococcal Antigens

<130> CHIR0159

<140> 09/302,626

<141> 1999-04-30

<150> PCT/IB99/00103

<151> 1999-01-14

<160> 195

<170> PatentIn Ver. 2.1

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<211> 736

<212> DNA

<213> Neisseria meningitidis

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cgtccgcact tacgacacag tcgagttcct gagcgcagat acgaaaacaa cgactgttaa 660
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 Glu Asn Ser Asp Trp Ala Val Tyr Phe Asn Glu Lys Gly Val Leu Thr
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 Ala Arg Glu Ile Thr Xaa Lys Ala Gly Asp Asn Leu Lys Ile Lys Gln
 65 70 75 80
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 100 105 110
 Val Asn Ile Thr Ser Asp Thr Lys Gly Leu Asn Phe Ala Lys Glu Thr
 115 120 125
 Ala Gly Thr Asn Gly Asp Thr Thr Val His Leu Asn Gly Ile Gly Ser
 130 135 140
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 195 200 205
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<212> PRT

<213> Neisseria meningitidis

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Ala Ser Ala Asn Asn Glu Glu Gln Glu Glu Asp Leu Tyr Leu Asp Pro
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435	440	445
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Ala Gln Leu Lys Gly Val Ala Gln Asn Leu Asn Asn Arg Ile Asp Asn 500 505 510		
Val Asp Gly Asn Ala Arg Ala Gly Ile Ala Gln Ala Ile Ala Thr Ala 515 520 525		
Gly Leu Val Gln Ala Tyr Leu Pro Gly Lys Ser Met Met Ala Ile Gly 530 535 540		
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 35 40 45
 Ala Asn Ala Thr Asp Glu Asp Glu Glu Glu Glu Leu Glu Ser Val Gln
 50 55 60
 Arg Ser Val Val Gly Ser Ile Gln Ala Ser Met Glu Gly Ser Gly Glu
 65 70 75 80
 Leu Glu Thr Ile Ser Leu Ser Met Thr Asn Asp Ser Lys Glu Phe Val
 85 90 95

Asp Pro Tyr Ile Val Val Thr Leu Lys Ala Gly Asp Asn Leu Lys Ile
 100 105 110
 Lys Gln Asn Thr Asn Glu Asn Thr Asn Ala Ser Ser Phe Thr Tyr Ser
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 130 135 140
 Ser Phe Gly Ala Asn Gly Lys Lys Val Asn Ile Ile Ser Asp Thr Lys
 145 150 155 160
 Gly Leu Asn Phe Ala Lys Glu Thr Ala Gly Thr Asn Gly Asp Thr Thr
 165 170 175
 Val His Leu Asn Gly Ile Gly Ser Thr Leu Thr Asp Thr Leu Ala Gly
 180 185 190
 Ser Ser Ala Ser His Val Asp Ala Gly Asn Xaa Ser Thr His Tyr Thr
 195 200 205
 Arg Ala Ala Ser Ile Lys Asp Val Leu Asn Ala Gly Trp Asn Ile Lys
 210 215 220
 Gly Val Lys Xaa Gly Ser Thr Thr Gly Gln Ser Glu Asn Val Asp Phe
 225 230 235 240
 Val Arg Thr Tyr Asp Thr Val Glu Phe Leu Ser Ala Asp Thr Xaa Thr
 245 250 255
 Thr Thr Val Asn Val Glu Ser Lys Asp Asn Gly Lys Arg Thr Glu Val
 260 265 270
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 275 280 285
 Val Thr Gly Lys Gly Lys Gly Glu Asn Gly Ser Ser Thr Asp Glu Gly
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 Glu Gly Leu Val Thr Ala Lys Glu Val Ile Asp Ala Val Asn Lys Ala
 305 310 315 320
 Gly Trp Arg Met Lys Thr Thr Thr Ala Asn Gly Gln Thr Gly Gln Ala
 325 330 335
 Asp Lys Phe Glu Thr Val Thr Ser Gly Thr Asn Val Thr Phe Ala Ser
 340 345 350
 Gly Lys Gly Thr Thr Ala Thr Val Ser Lys Asp Asp Gln Gly Asn Ile
 355 360 365
 Thr Val Met Tyr Asp Val Asn Val Gly Asp Ala Leu Asn Val Asn Gln
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 Leu Gln Asn Ser Gly Trp Asn Leu Asp Ser Lys Ala Val Ala Gly Ser
 385 390 395 400

Ser Gly Lys Val Ile Ser Gly Asn Val Ser Pro Ser Lys Gly Lys Met
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 Asn Gly Lys Asn Ile Asp Ile Ala Thr Ser Met Ala Pro Gln Phe Ser
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 Ser Val Ser Leu Gly Ala Gly Ala Asp Ala Pro Thr Leu Ser Val Asp
 450 455 460
 Asp Glu Gly Ala Leu Asn Val Gly Ser Lys Asp Ala Asn Lys Pro Val
 465 470 475 480
 Arg Ile Thr Asn Val Ala Pro Gly Val Lys Xaa Gly Asp Val Thr Asn
 485 490 495
 Val Xaa Gln Leu Lys Gly Val Ala Gln Asn Leu Asn Asn Arg Ile Asp
 500 505 510
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 515 520 525
 Ala Gly Leu Val Gln Ala Tyr Leu Pro Gly Lys Ser Met Met Ala Ile
 530 535 540
 Gly Gly Gly Thr Tyr Arg Gly Glu Ala Gly Tyr Ala Ile Gly Tyr Ser
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 35 40 45
 Ala Arg Gly Asp Val Gln Ile Pro Gln Asn Pro Glu Arg Ile Ala Val
 50 55 60
 Tyr Asp Leu Gly Met Leu Asp Thr Leu Ser Lys Leu Gly Val Lys Thr
 65 70 75 80
 Gly Leu Ser Val Asp Lys Asn Arg Leu Pro Tyr Leu Glu Glu Tyr Phe
 85 90 95
 Lys Thr Thr Lys Pro Ala Gly Thr Leu Phe Glu Pro Asp Tyr Glu Thr
 100 105 110
 Leu Asn Ala Tyr Lys Pro Gln Leu Ile Ile Ile Gly Ser Arg Ala Ala
 115 120 125
 Lys Ala Phe Asp Lys Leu Asn Glu Ile Ala Pro Thr Ile Xaa Xaa Thr
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 <213> Neisseria meningitidis

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 ggtttgtccg tcgataaaaa ccgcctgccg tatttagagg aatatttcaa aacgacaaaa 300

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<213> Neisseria meningitidis

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Ala Val Ser Ala Ala Gln Thr Glu Gly Ala Ser Val Thr Val Lys Thr
      35             40             45

Ala Arg Gly Asp Val Gln Ile Pro Gln Asn Pro Glu Arg Ile Ala Val
      50             55             60

Tyr Asp Leu Gly Met Leu Asp Thr Leu Ser Lys Leu Gly Val Lys Thr
      65             70             75             80

Gly Leu Ser Val Asp Lys Asn Arg Leu Pro Tyr Leu Glu Glu Tyr Phe
      85             90             95

Lys Thr Thr Lys Pro Ala Gly Thr Leu Phe Glu Pro Asp Tyr Glu Thr
      100            105            110

Leu Asn Ala Tyr Lys Pro Gln Leu Ile Ile Ile Gly Ser Arg Ala Ala
      115            120            125

Lys Ala Phe Asp Lys Leu Asn Glu Ile Ala Pro Thr Ile Glu Met Thr
      130            135            140

Ala Asp Thr Ala Asn Leu Lys Glu Ser Ala Lys Glu Arg Ile Asp Ala
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Leu Ala Gln Ile Phe Gly Lys Gln Ala Glu Ala Asp Lys Leu Lys Ala
      165            170            175

Glu Ile Asp Ala Ser Phe Glu Ala Ala Lys Thr Ala Ala Gln Gly Lys
      180            185            190

Gly Lys Gly Leu Val Ile Leu Val Asn Gly Gly Lys Met Ser Ala Phe

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Asp Arg Ser Ala Ala Ile Gly Glu Glu Gly Gln Ala Ala Lys Asp Val 260 265 270		
Leu Asp Asn Pro Leu Val Ala Glu Thr Thr Ala Trp Lys Lys Gly Gln 275 280 285		
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<210> 11
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 gccatcggcg aagaggggtca ggcggcgaaa gacgtgttga acaatccgct ggttgccgaa 840
 acaaccgctt ggaaaaaagg acaagtcgtt taccttggtc ctgaaactta tttggcagcc 900
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 <213> Neisseria meningitidis

<400> 12

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Ala	Cys	Ser	Pro	Gln	Asn	Ser	Asp	Ser	Ala	Pro	Gln	Ala	Lys	Glu	Gln	20	25	30	
Ala	Val	Ser	Ala	Ala	Gln	Ser	Glu	Gly	Val	Ser	Val	Thr	Val	Lys	Thr	35	40	45	
Ala	Arg	Gly	Asp	Val	Gln	Ile	Pro	Gln	Asn	Pro	Glu	Arg	Ile	Ala	Val	50	55	60	
Tyr	Asp	Leu	Gly	Met	Leu	Asp	Thr	Leu	Ser	Lys	Leu	Gly	Val	Lys	Thr	65	70	75	80
Gly	Leu	Ser	Val	Asp	Lys	Asn	Arg	Leu	Pro	Tyr	Leu	Glu	Glu	Tyr	Phe	85	90	95	
Lys	Thr	Thr	Lys	Pro	Ala	Gly	Thr	Leu	Phe	Glu	Pro	Asp	Tyr	Glu	Thr	100	105	110	
Leu	Asn	Ala	Tyr	Lys	Pro	Gln	Leu	Ile	Ile	Ile	Gly	Ser	Arg	Ala	Ala	115	120	125	
Lys	Ala	Phe	Asp	Lys	Leu	Asn	Glu	Ile	Ala	Pro	Thr	Ile	Glu	Met	Thr	130	135	140	
Ala	Asp	Thr	Ala	Asn	Leu	Lys	Glu	Ser	Ala	Lys	Glu	Arg	Ile	Asp	Ala	145	150	155	160
Leu	Ala	Gln	Ile	Phe	Gly	Lys	Lys	Ala	Glu	Ala	Asp	Lys	Leu	Lys	Ala	165	170	175	
Glu	Ile	Asp	Ala	Ser	Phe	Glu	Ala	Ala	Lys	Thr	Ala	Ala	Gln	Gly	Lys	180	185	190	
Gly	Lys	Gly	Leu	Val	Ile	Leu	Val	Asn	Gly	Gly	Lys	Met	Ser	Ala	Phe	195	200	205	
Gly	Pro	Ser	Ser	Arg	Leu	Gly	Gly	Trp	Leu	His	Lys	Asp	Ile	Gly	Val	210	215	220	
Pro	Ala	Val	Asp	Glu	Ala	Ile	Lys	Glu	Gly	Ser	His	Gly	Gln	Pro	Ile	225	230	235	240
Ser	Phe	Glu	Tyr	Leu	Lys	Glu	Lys	Asn	Pro	Asp	Trp	Leu	Phe	Val	Leu	245	250	255	
Asp	Arg	Ser	Ala	Ala	Ile	Gly	Glu	Glu	Gly	Gln	Ala	Ala	Lys	Asp	Val	260	265	270	
Leu	Asn	Asn	Pro	Leu	Val	Ala	Glu	Thr	Thr	Ala	Trp	Lys	Lys	Gly	Gln	275	280	285	
Val	Val	Tyr	Leu	Val	Pro	Glu	Thr	Tyr	Leu	Ala	Ala	Gly	Gly	Ala	Gln	290	295	300	

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 ggtaaaaaag tcaaagtaac ctacggcttc aacaaacagg gtctgaccac atacgcttcc 180
 gccgtcatca acggcaaacg cgtgcaaatt cctgtcaatt tggacaaatc cgacaatgtg 240
 gaaacattct acggcaaaga aggcggttat gttttgggta ccggcgtgat ggatggcaaa 300
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 20 25 30

Thr Val Ser Tyr Val Cys Gln Gln Gly Lys Lys Val Lys Val Thr Tyr
 35 40 45

Gly Phe Asn Lys Gln Gly Leu Thr Thr Tyr Ala Ser Ala Val Ile Asn
 50 55 60

Gly Lys Arg Val Gln Met Pro Val Asn Leu Asp Lys Ser Asp Asn Val
 65 70 75 80

Glu Thr Phe Tyr Gly Lys Glu Gly Gly Tyr Val Leu Gly Thr Gly Val
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gaaacattct acggcacaaga aggcgggttat gttttgggta ccggcgatgat ggatggcaaa 300
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35 40 45
Gly Phe Asn Lys Gln Gly Leu Thr Thr Tyr Ala Ser Ala Val Ile Asn
50 55 60
Gly Lys Arg Val Gln Met Pro Val Asn Leu Asp Lys Ser Asp Asn Val
65 70 75 80
Glu Thr Phe Tyr Gly Lys Glu Gly Gly Tyr Val Leu Gly Thr Gly Val
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 aagctggaat ccaactcgac cgtatggcaa aagcaggccg gaagcggcag cacggttgaa 180
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 35 40 45
 Trp Gln Lys Gln Ala Gly Ser Gly Ser Thr Val Glu Thr Leu Lys Leu
 50 55 60
 Pro Ser Phe Glu Gly Pro Ala Leu Pro Lys Leu Thr Ala Pro Gly Gly
 65 70 75 80
 Tyr Ile Ala Asp Ile Pro Lys Gly Asn Leu Lys Thr Glu Ile Glu Lys
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 Leu Ala Lys Gln Pro Glu Tyr Ala Tyr Leu Lys Gln Leu Gln Thr Val
 100 105 110
 Lys Asp Val Asn Trp Asn Gln Val Gln Leu Ala Tyr Asp Lys Trp Asp
 115 120 125
 Tyr Lys Gln Glu Gly Leu Thr Gly Ala Gly Ala Ala Ile Xaa Ala Leu
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<210> 19
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Ser	Lys	Asn	Glu	Leu	Asn	Glu	Thr	Lys	Leu	Pro	Val	Arg	Val	Ile	Ala		
		35					40					45					
Gln	Thr	Ala	Lys	Thr	Arg	Ser	Gly	Trp	Asp	Thr	Val	Leu	Glu	Gly	Thr		
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Glu	Phe	Lys	Thr	Thr	Leu	Ser	Gly	Ala	Asp	Ile	Gln	Ala	Gly	Val	Gly		
65					70					75					80		
Glu	Lys	Ala	Arg	Ala	Asp	Ala	Lys	Ile	Ile	Leu	Lys	Gly	Ile	Val	Asn		
			85					90						95			
Arg	Ile	Gln	Thr	Glu	Glu	Lys	Leu	Glu	Ser	Asn	Ser	Thr	Val	Trp	Gln		
		100						105					110				
Lys	Gln	Ala	Gly	Ser	Gly	Ser	Thr	Val	Glu	Thr	Leu	Lys	Leu	Pro	Ser		
	115						120					125					
Phe	Glu	Gly	Pro	Ala	Leu	Pro	Lys	Leu	Thr	Ala	Pro	Gly	Gly	Tyr	Ile		
130						135					140						
Ala	Asp	Ile	Pro	Lys	Gly	Asn	Leu	Lys	Thr	Glu	Ile	Glu	Lys	Leu	Ala		
145					150					155					160		
Lys	Gln	Pro	Glu	Tyr	Ala	Tyr	Leu	Lys	Gln	Leu	Gln	Thr	Val	Lys	Asp		
			165						170					175			
Val	Asn	Trp	Asn	Gln	Val	Gln	Leu	Ala	Tyr	Asp	Lys	Trp	Asp	Tyr	Lys		
		180						185					190				
Gln	Glu	Gly	Leu	Thr	Gly	Ala	Gly	Ala	Ala	Ile	Ile	Ala	Leu	Ala	Val		
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Thr	Val	Val	Thr	Ser	Gly	Ala	Gly	Thr	Gly	Ala	Val	Leu	Gly	Leu	Asn		
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Gly	Ala	Ala	Ala	Ala	Ala	Thr	Asp	Ala	Ala	Phe	Ala	Ser	Leu	Ala	Ser		
225					230					235					240		
Gln	Ala	Ser	Val	Ser	Phe	Ile	Asn	Asn	Lys	Gly	Asn	Ile	Gly	Asn	Thr		
			245						250					255			
Leu	Lys	Glu	Leu	Gly	Arg	Ser	Ser	Thr	Val	Lys	Asn	Leu	Met	Val	Ala		
		260						265					270				
Val	Ala	Thr	Ala	Gly	Val	Ala	Asp	Lys	Ile	Gly	Ala	Ser	Ala	Leu	Asn		
	275						280					285					
Asn	Val	Ser	Asp	Lys	Gln	Trp	Ile	Asn	Asn	Leu	Thr	Val	Asn	Leu	Ala		
	290					295					300						
Asn	Ala	Gly	Ser	Ala	Ala	Leu	Ile	Asn	Thr	Ala	Val	Asn	Gly	Gly	Ser		
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 595 600 605
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 Glu Phe Lys Thr Thr Leu Ala Gly Ala Asp Ile Gln Ala Gly Val Xaa
 65 70 75 80
 Glu Lys Ala Arg Val Asp Ala Lys Ile Ile Leu Lys Gly Ile Val Asn
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 Arg Ile Gln Ser Glu Glu Lys Leu Glu Thr Asn Ser Thr Val Trp Gln
 100 105 110

Lys Gln Ala Gly Arg Gly Ser Thr Ile Glu Thr Leu Lys Leu Pro Ser
 115 120 125
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 Val Asp Ile Pro Lys Gly Asn Leu Lys Thr Glu Ile Glu Lys Leu Ser
 145 150 155 160
 Lys Gln Pro Glu Tyr Ala Tyr Leu Lys Gln Leu Gln Val Ala Lys Asn
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 Ile Asn Trp Asn Gln Val Gln Leu Ala Tyr Asp Arg Trp Asp Tyr Lys
 180 185 190
 Gln Glu Gly Leu Thr Glu Ala Gly Ala Ala Ile Ile Ala Leu Ala Val
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 225 230 235 240
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 405 410 415

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 580 585 590
 Gln Asn Thr Pro Ile Thr Asn Val Lys Tyr Pro Glu Gly Ile Ser Phe
 595 600 605
 Asp Thr Asn Leu Xaa Arg His Leu Ala Asn Ala Asp Gly Phe Ser Gln
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 Glu Gln Gly Ile Lys Gly Ala His Asn Arg Thr Asn Xaa Met Ala Glu
 625 630 635 640
 Leu Asn Ser Arg Gly Gly Xaa Val Lys Ser Glu Thr Xaa Thr Asp Ile
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 Glu Gly Ile Thr Arg Ile Lys Tyr Glu Ile Pro Thr Leu Asp Arg Thr
 660 665 670
 Gly Lys Pro Asp Gly Gly Phe Lys Glu Ile Ser Ser Ile Lys Thr Val
 675 680 685
 Tyr Asn Pro Lys Xaa Phe Xaa Asp Asp Lys Ile Leu Gln Met Ala Gln
 690 695 700
 Xaa Ala Xaa Ser Gln Gly Tyr Ser Lys Ala Ser Lys Ile Ala Gln Asn
 705 710 715 720
 Glu Arg Thr Lys Ser Ile Ser Glu Arg Lys Asn Val Ile Gln Phe Ser

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Gly Arg Ile Thr Asn Ile His Pro Glu
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 gtcttgggaa cctttgtcca cccaacgcat atctgcctgc ggattctcat tgcgcttct 180
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 35 40 45
 Thr His Ile Cys Leu Arg Ile Leu Ile Ala Ala Ser Trp Leu Leu Ile
 50 55 60
 Phe Leu Pro Ser Arg Phe Ser Thr Ser Arg Leu Arg Ala Ser Ala Tyr
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 His Arg Gly Phe Ser Thr Leu Asp Val Val Ser Val Ala Leu Leu Val
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 100 105 110
 Gly Asp Thr Val Ala Arg Val Arg Glu Leu Glu Gln Ile Arg Asn Phe
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 <212> DNA
 <213> Neisseria meningitidis

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<211> 710
<212> PRT
<213> Neisseria meningitidis

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Glu Phe Cys Thr Ser Ala Gln Ser Asp Leu Asn Glu Thr Gln Trp Leu
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Leu Ala Ala Lys Ser Leu Gly Leu Lys Ala Lys Val Val Arg Gln Pro
      50             55             60

Ile Lys Arg Leu Ala Met Ala Thr Leu Pro Ala Leu Val Trp Cys Asp

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Ala Ser Arg Ala Ser Val Leu Gly Ser Leu Ala Lys Phe Asp Phe Thr	130	135	140
Trp Phe Ile Pro Ala Val Ile Lys Tyr Arg Arg Leu Phe Phe Glu Val	145	150	155
Leu Val Val Ser Val Val Leu Gln Leu Phe Ala Leu Ile Thr Pro Leu	165	170	175
Phe Phe Gln Val Val Met Asp Lys Val Leu Val His Arg Gly Phe Ser	180	185	190
Thr Leu Asp Val Val Ser Val Ala Leu Leu Val Val Ser Leu Phe Glu	195	200	205
Ile Val Leu Gly Gly Leu Arg Thr Tyr Leu Phe Ala His Thr Thr Ser	210	215	220
Arg Ile Asp Val Glu Leu Gly Ala Arg Leu Phe Arg His Leu Leu Ser	225	230	235
Leu Pro Leu Ser Tyr Phe Glu His Arg Arg Val Gly Asp Thr Val Ala	245	250	255
Arg Val Arg Glu Leu Glu Gln Ile Arg Asn Phe Leu Thr Gly Gln Ala	260	265	270
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Arg Leu Asn Asp Lys Phe Ala Arg Asn Ala Asp Asn Gln Ser Phe Leu	325	330	335
Val Glu Ser Ile Thr Ala Val Gly Thr Val Lys Ala Met Ala Val Glu	340	345	350
Pro Gln Met Thr Gln Arg Trp Asp Asn Gln Leu Ala Ala Tyr Val Ala	355	360	365
Ser Gly Phe Arg Val Thr Lys Leu Ala Val Val Gly Gln Gln Gly Val			

370	375	380
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Asn Met Leu Ser Gly Gln Val Ala Ala Pro Val Ile Arg Leu Ala Gln 420 425 430		
Leu Trp Gln Asp Phe Gln Gln Val Gly Ile Ser Val Ala Arg Leu Gly 435 440 445		
Asp Ile Leu Asn Ala Pro Thr Glu Asn Ala Ser Ser His Leu Ala Leu 450 455 460		
Pro Asp Ile Arg Gly Glu Ile Thr Phe Glu His Val Asp Phe Arg Tyr 465 470 475 480		
Lys Ala Asp Gly Arg Leu Ile Leu Gln Asp Leu Asn Leu Arg Ile Arg 485 490 495		
Ala Gly Glu Val Leu Gly Ile Val Gly Arg Ser Gly Ser Gly Lys Ser 500 505 510		
Thr Leu Thr Lys Leu Val Gln Arg Leu Tyr Val Pro Glu Gln Gly Arg 515 520 525		
Val Leu Val Asp Gly Asn Asp Leu Ala Leu Ala Ala Pro Ala Trp Leu 530 535 540		
Arg Arg Gln Val Gly Val Val Leu Gln Glu Asn Val Leu Leu Asn Arg 545 550 555 560		
Ser Ile Arg Asp Asn Ile Ala Leu Thr Asp Thr Gly Met Pro Leu Glu 565 570 575		
Arg Ile Ile Glu Ala Ala Lys Leu Ala Gly Ala His Glu Phe Ile Met 580 585 590		
Glu Leu Pro Glu Gly Tyr Gly Thr Val Val Gly Glu Gln Gly Ala Gly 595 600 605		
Leu Ser Gly Gly Gln Arg Gln Arg Ile Ala Ile Ala Arg Ala Leu Ile 610 615 620		
Thr Asn Pro Arg Ile Leu Ile Phe Asp Glu Ala Thr Ser Ala Leu Asp 625 630 635 640		
Tyr Glu Ser Glu Arg Ala Ile Met Gln Asn Met Gln Ala Ile Cys Ala 645 650 655		
Asn Arg Thr Val Leu Ile Ile Ala His Arg Leu Ser Thr Val Lys Thr 660 665 670		
Ala His Arg Ile Ile Ala Met Asp Lys Gly Arg Ile Val Glu Ala Gly		

675	680	685
Thr Gln Gln Glu Leu Leu Ala Lys Pro Asn Gly Tyr Tyr Arg Tyr Leu		
690	695	700

Tyr Asp Leu Gln Asn Gly
705 710
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tttgacttta cctgggttat tccggcggtta atcaaatacc gccgggttgtt ttttgaagta 480
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ttgttggtgg tgcgctgtt tgagattgtg ttgggcggtt tgcggacgta tctgtttgca 660
catacgactt cacgtattga tgtggaattg ggcgcgcgtt tgttccggca tctgctttcc 720
ctgcctttat cctatttcga gcacagacga gtgggtgata cgggtggctcg ggtgcgggaa 780
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ttggcttcgt tgcctgccta tgcgttttgg tgcgcattta tcagtccgat actgcggacg 960
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aatcagttgg cggcttatgt ggcttcggga tttcgggtaa cgaagttggc ggtggtcggc 1140
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gcagccaaac tggcggggcg acacgagttt attatggagc tgcgggaagg ctacggcacc 1800
gtggtggggc aacaagggcg cggcttgtcg ggcggacagc ggcagcgtat tgcgattgcc 1860
cgcgcggtta tcaccaatcc gcgcattctg atttttgatg aagccaccag cgcgctggat 1920
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ctgattatcg cccaccgtct gtccactgtt aaaacggcac accggatcat tgccatggat 2040
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taccgctatc tgtatgattt acagaacggg tag 2133

<210> 30
<211> 710
<212> PRT
<213> Neisseria meningitidis

<400> 30

Met	Ser	Ile	Val	Ser	Ala	Pro	Leu	Pro	Ala	Leu	Ser	Ala	Leu	Ile	Ile
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Leu	Ala	His	Tyr	His	Gly	Ile	Ala	Ala	Asn	Pro	Ala	Asp	Ile	Gln	His
			20					25					30		
Glu	Phe	Cys	Thr	Ser	Ala	Gln	Ser	Asp	Leu	Asn	Glu	Thr	Gln	Trp	Leu
		35					40					45			
Leu	Ala	Ala	Lys	Ser	Leu	Gly	Leu	Lys	Ala	Lys	Val	Val	Arg	Gln	Pro
	50					55					60				
Ile	Lys	Arg	Leu	Ala	Met	Ala	Thr	Leu	Pro	Ala	Leu	Val	Trp	Cys	Asp
65					70					75					80
Asp	Gly	Asn	His	Phe	Ile	Leu	Ala	Lys	Thr	Asp	Gly	Gly	Gly	Glu	His
				85					90					95	
Ala	Gln	Tyr	Leu	Ile	Gln	Asp	Leu	Thr	Thr	Asn	Lys	Ser	Ala	Val	Leu
			100					105					110		
Ser	Phe	Ala	Glu	Phe	Ser	Asn	Arg	Tyr	Ser	Gly	Lys	Leu	Ile	Leu	Val
		115					120					125			
Ala	Ser	Arg	Ala	Ser	Val	Leu	Gly	Ser	Leu	Ala	Lys	Phe	Asp	Phe	Thr
	130					135					140				
Trp	Phe	Ile	Pro	Ala	Val	Ile	Lys	Tyr	Arg	Arg	Leu	Phe	Phe	Glu	Val
145					150					155					160
Leu	Val	Val	Ser	Val	Val	Leu	Gln	Leu	Phe	Ala	Leu	Ile	Thr	Pro	Leu
				165					170					175	
Phe	Phe	Gln	Val	Val	Met	Asp	Lys	Val	Leu	Val	His	Arg	Gly	Phe	Ser
			180					185					190		
Thr	Leu	Asp	Val	Val	Ser	Val	Ala	Leu	Leu	Val	Val	Ser	Leu	Phe	Glu
		195					200					205			
Ile	Val	Leu	Gly	Gly	Leu	Arg	Thr	Tyr	Leu	Phe	Ala	His	Thr	Thr	Ser
	210					215					220				
Arg	Ile	Asp	Val	Glu	Leu	Gly	Ala	Arg	Leu	Phe	Arg	His	Leu	Leu	Ser
225					230					235					240
Leu	Pro	Leu	Ser	Tyr	Phe	Glu	His	Arg	Arg	Val	Gly	Asp	Thr	Val	Ala
				245					250					255	
Arg	Val	Arg	Glu	Leu	Glu	Gln	Ile	Arg	Asn	Phe	Leu	Thr	Gly	Gln	Ala
			260					265					270		
Leu	Thr	Ser	Val	Leu	Asp	Leu	Ala	Phe	Ser	Phe	Ile	Phe	Leu	Ala	Val
		275					280					285			
Met	Trp	Tyr	Tyr	Ser	Ser	Thr	Leu	Thr	Trp	Val	Val	Leu	Ala	Ser	Leu
	290					295					300				

Pro Ala Tyr Ala Phe Trp Ser Ala Phe Ile Ser Pro Ile Leu Arg Thr
 305 310 315 320
 Arg Leu Asn Asp Lys Phe Ala Arg Asn Ala Asp Asn Gln Ser Phe Leu
 325 330 335
 Val Glu Ser Ile Thr Ala Val Gly Thr Val Lys Ala Met Ala Val Glu
 340 345 350
 Pro Gln Met Thr Gln Arg Trp Asp Asn Gln Leu Ala Ala Tyr Val Ala
 355 360 365
 Ser Gly Phe Arg Val Thr Lys Leu Ala Val Val Gly Gln Gln Gly Val
 370 375 380
 Gln Leu Ile Gln Lys Leu Val Thr Val Ala Thr Leu Trp Ile Gly Ala
 385 390 395 400
 Arg Leu Val Ile Glu Ser Lys Leu Thr Val Gly Gln Leu Ile Ala Phe
 405 410 415
 Asn Met Leu Ser Gly Gln Val Ala Ala Pro Val Ile Arg Leu Ala Gln
 420 425 430
 Leu Trp Gln Asp Phe Gln Gln Val Gly Ile Ser Val Ala Arg Leu Gly
 435 440 445
 Asp Ile Leu Asn Ala Pro Thr Glu Asn Ala Ser Ser His Leu Ala Leu
 450 455 460
 Pro Asp Ile Arg Gly Glu Ile Thr Phe Glu His Val Asp Phe Arg Tyr
 465 470 475 480
 Lys Ala Asp Gly Arg Leu Ile Leu Gln Asp Leu Asn Leu Arg Ile Arg
 485 490 495
 Ala Gly Glu Val Leu Gly Ile Val Gly Arg Ser Gly Ser Gly Lys Ser
 500 505 510
 Thr Leu Thr Lys Leu Val Gln Arg Leu Tyr Val Pro Ala Gln Gly Arg
 515 520 525
 Val Leu Val Asp Gly Asn Asp Leu Ala Leu Ala Ala Pro Ala Trp Leu
 530 535 540
 Arg Arg Gln Val Gly Val Val Leu Gln Glu Asn Val Leu Leu Asn Arg
 545 550 555 560
 Ser Ile Arg Asp Asn Ile Ala Leu Thr Asp Thr Gly Met Pro Leu Glu
 565 570 575
 Arg Ile Ile Glu Ala Ala Lys Leu Ala Gly Ala His Glu Phe Ile Met
 580 585 590
 Glu Leu Pro Glu Gly Tyr Gly Thr Val Val Gly Glu Gln Gly Ala Gly
 595 600 605
 Leu Ser Gly Gly Gln Arg Gln Arg Ile Ala Ile Ala Arg Ala Leu Ile

<211> 261
<212> DNA
<213> *Neisseria meningitidis*

<400> 33
atgaaatact tgatccgcac cgccttactc gcagtcgcag ccgccggcat ctacgcctgc 60
caaccgcaat ccgaagccgc agtgcaagtc aaggctgaaa acagcctgac cgctatgcgc 120
ttagccgtcg ccgacaaaca ggcagagatt gacgggttga acgcccacaaat cgacgccgaa 180
atcagacaac gcgaagccga agaattgaaa gactaccgat ggatacacgg cgacgcggaa 240
gtgccggagc tggaaaaatg a 261

<210> 34
<211> 86
<212> PRT
<213> *Neisseria meningitidis*

<400> 34
Met Lys Tyr Leu Ile Arg Thr Ala Leu Leu Ala Val Ala Ala Ala Gly
1 5 10 15
Ile Tyr Ala Cys Gln Pro Gln Ser Glu Ala Ala Val Gln Val Lys Ala
20 25 30
Glu Asn Ser Leu Thr Ala Met Arg Leu Ala Val Ala Asp Lys Gln Ala
35 40 45
Glu Ile Asp Gly Leu Asn Ala Gln Ile Asp Ala Glu Ile Arg Gln Arg
50 55 60
Glu Ala Glu Glu Leu Lys Asp Tyr Arg Trp Ile His Gly Asp Ala Glu
65 70 75 80
Val Pro Glu Leu Glu Lys
85

<210> 35
<211> 279
<212> DNA
<213> *Neisseria meningitidis*

<400> 35
atggttatcg gaatattact cgcacaaagc aagcatgctc ttgtcattac tctattgtta 60
aatcccgtct tccatgcac cagttgcgta tcgcgttsgg caatacggaa taaaatctgc 120
tgttctgctt tggctaaatt tgccaaattg tttattgttt ctttaggagc agcttgctta 180
gccgccttcg ctttcgacaa cgccccacaa ggcgcttccc aagcgttgcc taccgttacc 240
gcacccgtgg cgattcccgc gcccgcttcg gcagcctga 279

<210> 36
<211> 92
<212> PRT
<213> *Neisseria meningitidis*

<220>
<221> SITE

<222> (33)
<223> unknown

<400> 36

Met Val Ile Gly Ile Leu Leu Ala Ser Ser Lys His Ala Leu Val Ile
1 5 10 15

Thr Leu Leu Leu Asn Pro Val Phe His Ala Ser Ser Cys Val Ser Arg
20 25 30

Xaa Ala Ile Arg Asn Lys Ile Cys Cys Ser Ala Leu Ala Lys Phe Ala
35 40 45

Lys Leu Phe Ile Val Ser Leu Gly Ala Ala Cys Leu Ala Ala Phe Ala
50 55 60

Phe Asp Asn Ala Pro Thr Gly Ala Ser Gln Ala Leu Pro Thr Val Thr
65 70 75 80

Ala Pro Val Ala Ile Pro Ala Pro Ala Ser Ala Ala
85 90

<210> 37

<211> 312

<212> DNA

<213> Neisseria meningitidis

<400> 37

atggccttgta caggcttgat ggtttttccg ttaatgggta tcggaatatt acttgcacatca 60
agcaagcctg ctccctttcct tactctattg ttaaatacccg tcttccatgc atccagttgc 120
gtatcgcggtt gggcaatacgc gaataaaaatc tgctgttctg ctttgggctaa atttgccaaa 180
ttgtttattg tttcttttagg agcagcttgc ttagccgcct tcgctttcga caacgcccc 240
acaggcgctt cccaagcggtt gcctaccggtt accgcacccg tggcgattcc cgcgccccgct 300
tcggcagcct ga 312

<210> 38

<211> 103

<212> PRT

<213> Neisseria meningitidis

<400> 38

Met Ala Cys Thr Gly Leu Met Val Phe Pro Leu Met Val Ile Gly Ile
1 5 10 15

Leu Leu Ala Ser Ser Lys Pro Ala Pro Phe Leu Thr Leu Leu Leu Asn
20 25 30

Pro Val Phe His Ala Ser Ser Cys Val Ser Arg Trp Ala Ile Arg Asn
35 40 45

Lys Ile Cys Cys Ser Ala Leu Ala Lys Phe Ala Lys Leu Phe Ile Val
50 55 60

Ser Leu Gly Ala Ala Cys Leu Ala Ala Phe Ala Phe Asp Asn Ala Pro
65 70 75 80

Thr Gly Ala Ser Gln Ala Leu Pro Thr Val Thr Ala Pro Val Ala Ile
 85 90 95

Pro Ala Pro Ala Ser Ala Ala
 100

<210> 39
 <211> 255
 <212> DNA
 <213> Neisseria meningitidis

<400> 39
 atgttcagta ttttaaagt gtttcttcat tgtattctgg cttgtgtagt ctctggtag 60
 acgcctacta tatttggtat ccttgctctt ttttacttat tgtatctttc ttatcttgct 120
 gtttttaaga ttttcttttc ttttttctta gacagagttt cactccgggc tcccaggctg 180
 gagtgcaaat ggcattgaccc ttgggtcac tggtcacgg ccacttctgc tattctgccg 240
 cctcagcctc caggg 255

<210> 40
 <211> 85
 <212> PRT
 <213> Neisseria meningitidis

<400> 40
 Met Phe Ser Ile Leu Asn Val Phe Leu His Cys Ile Leu Ala Cys Val
 1 5 10 15
 Val Ser Gly Glu Thr Pro Thr Ile Phe Gly Ile Leu Ala Leu Phe Tyr
 20 25 30
 Leu Leu Tyr Leu Ser Tyr Leu Ala Val Phe Lys Ile Phe Phe Ser Phe
 35 40 45
 Phe Leu Asp Arg Val Ser Leu Arg Ser Pro Arg Leu Glu Cys Lys Trp
 50 55 60
 His Asp Pro Leu Ala His Trp Leu Thr Ala Thr Ser Ala Ile Leu Pro
 65 70 75 80
 Pro Gln Pro Pro Gly
 85

<210> 41
 <211> 237
 <212> DNA
 <213> Neisseria meningitidis

<400> 41
 gtgcggacgt ggttggtttt ttggttgcag cgtttgaaat acccgttggt gctttggatt 60
 gcggatatgt tgctgtaccg gttgttgggc ggccgggaaa tcgaatgcgg ccgttgccct 120
 gtgccgccga tgacggattg gcagcatttt ttgccggcga tgggaacggg gtcggcttgg 180
 gtggcggtga tttgggcata cctgatgatt gaaagtgaat aaaacggaag atattga 237

<210> 42
 <211> 78
 <212> PRT
 <213> Neisseria meningitidis

<400> 42
 Val Arg Thr Trp Leu Val Phe Trp Leu Gln Arg Leu Lys Tyr Pro Leu
 1 5 10 15
 Leu Leu Trp Ile Ala Asp Met Leu Leu Tyr Arg Leu Leu Gly Gly Ala
 20 25 30
 Glu Ile Glu Cys Gly Arg Cys Pro Val Pro Pro Met Thr Asp Trp Gln
 35 40 45
 His Phe Leu Pro Ala Met Gly Thr Val Ser Ala Trp Val Ala Val Ile
 50 55 60
 Trp Ala Tyr Leu Met Ile Glu Ser Glu Lys Asn Gly Arg Tyr
 65 70 75

<210> 43
 <211> 237
 <212> DNA
 <213> Neisseria meningitidis

<400> 43
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 gcggatatgc tgctgtaccg gttgttgggc ggcgcggaaa tcgaatgcgg ccgttgccct 120
 gtaccgccga tgacggattg gcagcatttt ttgccgacga tgggaacggt ggcggccttg 180
 gtggcggtga tttgggcata cctgatgatt gaaagtgaaa aaaacggaag atattga 237

<210> 44
 <211> 78
 <212> PRT
 <213> Neisseria meningitidis

<400> 44
 Val Arg Thr Trp Leu Val Phe Trp Leu Gln Arg Leu Lys Tyr Pro Leu
 1 5 10 15
 Leu Leu Cys Ile Ala Asp Met Leu Leu Tyr Arg Leu Leu Gly Gly Ala
 20 25 30
 Glu Ile Glu Cys Gly Arg Cys Pro Val Pro Pro Met Thr Asp Trp Gln
 35 40 45
 His Phe Leu Pro Thr Met Gly Thr Val Ala Ala Trp Val Ala Val Ile
 50 55 60
 Trp Ala Tyr Leu Met Ile Glu Ser Glu Lys Asn Gly Arg Tyr
 65 70 75

<210> 45
 <211> 660

<212> DNA
 <213> Neisseria meningitidis

<400> 45
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 attaccgtct cgcacgtggc gcgcggctat acggcgcgct actggggaga caacactgcc 120
 gaacaatacg gcaggctgac actgaacccc ctgccccata tcgatttggt cggcacaatc 180
 atcgtaccgc tgcttacttt gatgttcacg cccttcctgt tcggctgggc gcgtccgatt 240
 cctatcgatt cgcgcaactt ccgcaaccgg cgccttgcct ggcgttgctg tgccgcgtcc 300
 ggcccgtgt cgaatctagc gatggctgtw ctgtggggcg tggttttggt gctgactccg 360
 tatgtcggcg gggcgtatca gatgccgttg gctcaaattg caaactacgg tattctgatc 420
 aatgcgattc tggtcgcgct caacatcatc cccatcctgc cttgggacgg cggcattttc 480
 atcgacacct tcctgtcggc gaaatattcg caagcgttcc gcaaaatcga accttatggg 540
 acgtggatta tcctactgct gatgctgacc sgggttttgg gtgcgtttat wgcaccgatt 600
 stgcggmtgc gtgattgcrt ttgtgcagat gtwcgtctga ctggctttca gacggcataa 660

<210> 46
 <211> 219
 <212> PRT
 <213> Neisseria meningitidis

<220>
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 <222> (191)
 <223> unknown

<220>
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 <222> (201)
 <223> unknown

<220>
 <221> SITE
 <222> (203)
 <223> unknown

<220>
 <221> SITE
 <222> (207)
 <223> unknown

<400> 46
 Met Phe Gln Asn Phe Asp Leu Gly Val Phe Leu Leu Ala Val Leu Pro
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 Val Leu Pro Ser Ile Thr Val Ser His Val Ala Arg Gly Tyr Thr Ala
 20 25 30
 Arg Tyr Trp Gly Asp Asn Thr Ala Glu Gln Tyr Gly Arg Leu Thr Leu
 35 40 45
 Asn Pro Leu Pro His Ile Asp Leu Val Gly Thr Ile Ile Val Pro Leu
 50 55 60
 Leu Thr Leu Met Phe Thr Pro Phe Leu Phe Gly Trp Ala Arg Pro Ile
 65 70 75 80

Pro Ile Asp Ser Arg Asn Phe Arg Asn Pro Arg Leu Ala Trp Arg Cys
 85 90 95
 Val Ala Ala Ser Gly Pro Leu Ser Asn Leu Ala Met Ala Val Leu Trp
 100 105 110
 Gly Val Val Leu Val Leu Thr Pro Tyr Val Gly Gly Ala Tyr Gln Met
 115 120 125
 Pro Leu Ala Gln Met Ala Asn Tyr Gly Ile Leu Ile Asn Ala Ile Leu
 130 135 140
 Phe Ala Leu Asn Ile Ile Pro Ile Leu Pro Trp Asp Gly Gly Ile Phe
 145 150 155 160
 Ile Asp Thr Phe Leu Ser Ala Lys Tyr Ser Gln Ala Phe Arg Lys Ile
 165 170 175
 Glu Pro Tyr Gly Thr Trp Ile Ile Leu Leu Leu Met Leu Thr Xaa Val
 180 185 190
 Leu Gly Ala Phe Ile Ala Pro Ile Xaa Arg Xaa Arg Asp Cys Xaa Cys
 195 200 205
 Ala Asp Val Arg Leu Thr Gly Phe Gln Thr Ala
 210 215

<210> 47
 <211> 639
 <212> DNA
 <213> Neisseria meningitidis

<400> 47
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 attaccgtca gggaggtggc gcgcggctat acggcgcgct actggggaga caacactgcc 120
 gaacaatacg gcaggctgac actgaacccc ctgccccata tcgatttggt cggcacaatc 180
 atcgtaaccg tgcttacttt gatgttcacg cccttcctgt tcggctgggc gcgtccgatt 240
 cctatcgatt cgcgcaactt ccgcaaccgg cgccttgccg ggcgttgctg tgccgcgtcc 300
 ggcccgcgtg cgaatctagc gatggctgtt ctgtggggcg tggttttggg gctgactccg 360
 tatgtcggcg gggcgatatca gatgccgttg gctcaaattg caaactacgg tattctgata 420
 aatgcgattc tgttcgcgct caacatcatc cccatcctgc cttagggacgg cggcattttc 480
 atcgacacct tctgtcggc gaaatattcg caagcgttcc gcaaaatcga accttatggg 540
 acgtggatta tctactgct gatgctgacc ggggttttgg gtgcgtttat tgcaccgatt 600
 gtgcggctgg tgattgcgtt tgtgcagatg ttctgtctga 639

<210> 48
 <211> 212
 <212> PRT
 <213> Neisseria meningitidis

<400> 48
 Met Phe Gln Asn Phe Asp Leu Gly Val Phe Leu Leu Ala Val Leu Pro
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Val Leu Leu Ser Ile Thr Val Arg Glu Val Ala Arg Gly Tyr Thr Ala
 20 25 30
 Arg Tyr Trp Gly Asp Asn Thr Ala Glu Gln Tyr Gly Arg Leu Thr Leu
 35 40 45
 Asn Pro Leu Pro His Ile Asp Leu Val Gly Thr Ile Ile Val Pro Leu
 50 55 60
 Leu Thr Leu Met Phe Thr Pro Phe Leu Phe Gly Trp Ala Arg Pro Ile
 65 70 75 80
 Pro Ile Asp Ser Arg Asn Phe Arg Asn Pro Arg Leu Ala Trp Arg Cys
 85 90 95
 Val Ala Ala Ser Gly Pro Leu Ser Asn Leu Ala Met Ala Val Leu Trp
 100 105 110
 Gly Val Val Leu Val Leu Thr Pro Tyr Val Gly Gly Ala Tyr Gln Met
 115 120 125
 Pro Leu Ala Gln Met Ala Asn Tyr Gly Ile Leu Ile Asn Ala Ile Leu
 130 135 140
 Phe Ala Leu Asn Ile Ile Pro Ile Leu Pro Trp Asp Gly Gly Ile Phe
 145 150 155 160
 Ile Asp Thr Phe Leu Ser Ala Lys Tyr Ser Gln Ala Phe Arg Lys Ile
 165 170 175
 Glu Pro Tyr Gly Thr Trp Ile Ile Leu Leu Leu Met Leu Thr Gly Val
 180 185 190
 Leu Gly Ala Phe Ile Ala Pro Ile Val Arg Leu Val Ile Ala Phe Val
 195 200 205
 Gln Met Phe Val
 210

<210> 49
 <211> 558
 <212> DNA
 <213> Neisseria meningitidis

<220>
 <221> misc_feature
 <222> (312)
 <223> any nucleotide

<220>
 <221> misc_feature
 <222> (328)..(330)
 <223> any nucleotide

<220>
 <221> misc_feature

<222> (353)
<223> any nucleotide

<220>
<221> misc_feature
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<223> any nucleotide

<220>
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<222> (426)
<223> any nucleotide

<220>
<221> misc_feature
<222> (473)
<223> any nucleotide

<220>
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<222> (506)
<223> any nucleotide

<400> 49
cgcggtata cagcgcgcta ctgggggtgac aacactgccg aacaatacgg caggctgaca 60
ctgaaccccc tgccccatat cgatttggtc ggcacaatca tcgtaccgct gcttactttg 120
atgttttacgc ccttcctggt cggtcgggcg cgtccgattc ctatcgattc gcgcaacttc 180
cgcaaccgcg gccttgccctg gcgttgcggt gccgcgtccg gcccgctgtc gaatctggcg 240
atggctgttc tgtggggcgt gggttttggtg ctgactccgt atgtcgggtg ggcgtatcag 300
atgccgttgg cncaaatggc aaactacnnn attctgatca atgcgattct gtncgcgctc 360
aacatcatcc ccatoctgcc ttggggacggc ggcattttca tcgacacctt cctgtcggcn 420
aaatantcgc aagcggttccg caaaatcgaa ccttatggga cgtggattat ccngctgctt 480
atgctgaccg ggggttttggg tgcgtntatt gcaccgattg tgcagctggt gattgcgttt 540
gtgcagatgt tcgtctga 558

<210> 50
<211> 185
<212> PRT
<213> Neisseria meningitidis

<220>
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<222> (110)
<223> unknown

<220>
<221> SITE
<222> (118)
<223> unknown

<220>
<221> SITE
<222> (142)
<223> unknown

<220>

<221> SITE
 <222> (158)
 <223> unknown

<220>
 <221> SITE
 <222> (169)
 <223> unknown

<400> 50
 Arg Gly Tyr Thr Ala Arg Tyr Trp Gly Asp Asn Thr Ala Glu Gln Tyr
 1 5 10 15
 Gly Arg Leu Thr Leu Asn Pro Leu Pro His Ile Asp Leu Val Gly Thr
 20 25 30
 Ile Ile Val Pro Leu Leu Thr Leu Met Phe Thr Pro Phe Leu Phe Gly
 35 40 45
 Trp Ala Arg Pro Ile Pro Ile Asp Ser Arg Asn Phe Arg Asn Pro Arg
 50 55 60
 Leu Ala Trp Arg Cys Val Ala Ala Ser Gly Pro Leu Ser Asn Leu Ala
 65 70 75 80
 Met Ala Val Leu Trp Gly Val Val Leu Val Leu Thr Pro Tyr Val Gly
 85 90 95
 Gly Ala Tyr Gln Met Pro Leu Ala Gln Met Ala Asn Tyr Xaa Ile Leu
 100 105 110
 Ile Asn Ala Ile Leu Xaa Ala Leu Asn Ile Ile Pro Ile Leu Pro Trp
 115 120 125
 Asp Gly Gly Ile Phe Ile Asp Thr Phe Leu Ser Ala Lys Xaa Ser Gln
 130 135 140
 Ala Phe Arg Lys Ile Glu Pro Tyr Gly Thr Trp Ile Ile Xaa Leu Leu
 145 150 155 160
 Met Leu Thr Gly Val Leu Gly Ala Xaa Ile Ala Pro Ile Val Gln Leu
 165 170 175
 Val Ile Ala Phe Val Gln Met Phe Val
 180 185

<210> 51
 <211> 498
 <212> DNA
 <213> Neisseria meningitidis

<400> 51
 atgaacctga tttcacgtta catcatccgt caaatggcgg ttatggcggg ttacgcgctc 60
 cttgccttcc tcgctttgta cagctttttt gaaatcctgt acgaaaccgg caacctcggc 120
 aaaggcagtt acggcatatg ggaaatgctg ggctacaccg ccctcaaaat gcccgcgccg 180
 gcctacgaac tgattcccct cgccgtcctt atcggcggac tgggtctccct cagccagctt 240

gccgcccggca gcgaactgac cgtcatcaaa gccagcggca tgagcaccaa aaagctgctg 300
 ttgattctgt cgcagttcgg ttttattttt gctattgcca ccgtcgcgct cggcgaatgg 360
 gttgcgcccc cactgagcca aaaagccgaa aacatcaaag ccgccgccat caacggcaaa 420
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<210> 52
 <211> 166
 <212> PRT
 <213> Neisseria meningitidis

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 Leu Tyr Glu Thr Gly Asn Leu Gly Lys Gly Ser Tyr Gly Ile Trp Glu
 35 40 45
 Met Leu Gly Tyr Thr Ala Leu Lys Met Pro Ala Arg Ala Tyr Glu Leu
 50 55 60
 Ile Pro Leu Ala Val Leu Ile Gly Gly Leu Val Ser Leu Ser Gln Leu
 65 70 75 80
 Ala Ala Gly Ser Glu Leu Thr Val Ile Lys Ala Ser Gly Met Ser Thr
 85 90 95
 Lys Lys Leu Leu Leu Ile Leu Ser Gln Phe Gly Phe Ile Phe Ala Ile
 100 105 110
 Ala Thr Val Ala Leu Gly Glu Trp Val Ala Pro Thr Leu Ser Gln Lys
 115 120 125
 Ala Glu Asn Ile Lys Ala Ala Ala Ile Asn Gly Lys Ile Ser Thr Gly
 130 135 140
 Asn Thr Gly Leu Trp Leu Lys Glu Lys Asn Ser Val Ile Asn Val Arg
 145 150 155 160
 Glu Met Leu Pro Asp His
 165

<210> 53
 <211> 980
 <212> DNA
 <213> Neisseria meningitidis

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 aaaggcagtt acggcatatg ggaaatgctg ggctacaccg cctcaaaaat gcccggccgc 180
 gcctacgaac tgattcccct cgcggtcctt atcggcggac tggctcctc cagccagctt 240
 gccgcccggca gcgaactgac cgtcatcaaa gccagcggca tgagcaccaa aaagctgctg 300

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atcagcaccg gcaataccgg cctttggctg aaagaaaaaa acagcrtkat caatgtgcgc 480
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gaattggcag aggcagtggg agccgattcc gccgttttga acagcgacgg cagttggcag 600
ttgaaaaaca tccgccgcag cacgcttggc gaagacaaaag tcgaggtctc tattgcggct 660
gaagaaaact ggccgatttc cgtcaaacgc aacctgatgg acgtattgct cgtcaaaccc 720
gaccaaagt ccgtcggcga actgaccacc tacatccgcc acctccaaaa caacagccaa 780
aacacccgaa tctacgccat cgcattgtgg cgcaaattgg tttaccccg cgcagcctgg 840
gtgatggcgc tcgtcgctt tgcctttacc ccgcaaacca cccgccacgg caatatgggc 900
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<210> 54
<211> 326
<212> PRT
<213> Neisseria meningitidis

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             20             25             30
Leu Tyr Glu Thr Gly Asn Leu Gly Lys Gly Ser Tyr Gly Ile Trp Glu
             35             40             45

Met Leu Gly Tyr Thr Ala Leu Lys Met Pro Ala Arg Ala Tyr Glu Leu
             50             55             60

Ile Pro Leu Ala Val Leu Ile Gly Gly Leu Val Ser Leu Ser Gln Leu
             65             70             75             80

Ala Ala Gly Ser Glu Leu Thr Val Ile Lys Ala Ser Gly Met Ser Thr
             85             90             95

Lys Lys Leu Leu Leu Ile Leu Ser Gln Phe Gly Phe Ile Phe Ala Ile
             100            105            110

Ala Thr Val Ala Leu Gly Glu Trp Val Ala Pro Thr Leu Ser Gln Lys
             115            120            125

Ala Glu Asn Ile Lys Ala Ala Ile Asn Gly Lys Ile Ser Thr Gly
             130            135            140

Asn Thr Gly Leu Trp Leu Lys Glu Lys Asn Ser Xaa Ile Asn Val Arg

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145		150		155		160
Glu Met Leu Pro Asp His Thr Leu Leu Gly Ile Lys Ile Trp Ala Arg						
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Asn Asp Lys Asn Glu Leu Ala Glu Ala Val Glu Ala Asp Ser Ala Val						
	180		185		190	
Leu Asn Ser Asp Gly Ser Trp Gln Leu Lys Asn Ile Arg Arg Ser Thr						
	195		200		205	
Leu Gly Glu Asp Lys Val Glu Val Ser Ile Ala Ala Glu Glu Asn Trp						
	210		215		220	
Pro Ile Ser Val Lys Arg Asn Leu Met Asp Val Leu Leu Val Lys Pro						
225		230		235		240
Asp Gln Met Ser Val Gly Glu Leu Thr Thr Tyr Ile Arg His Leu Gln						
	245		250		255	
Asn Asn Ser Gln Asn Thr Arg Ile Tyr Ala Ile Ala Trp Trp Arg Lys						
	260		265		270	
Leu Val Tyr Pro Ala Ala Ala Trp Val Met Ala Leu Val Ala Phe Ala						
	275		280		285	
Phe Thr Pro Gln Thr Thr Arg His Gly Asn Met Gly Leu Lys Leu Phe						
	290		295		300	
Gly Gly Ile Cys Xaa Gly Leu Leu Phe His Leu Ala Gly Arg Leu Phe						
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Gly Phe Thr Ser Gln Leu						
	325					

<210> 55
 <211> 1071
 <212> DNA
 <213> Neisseria meningitidis

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 aaaggcagtt acggcatatg ggaaatgntg ggntacaccg ccctcaaaat gnccgcccgc 180
 gcctacgaac tgatgcccct cgccgtcctt atcggcggac tggctctnt cagccagctt 240
 gccgccggca gcgaactgan cgtcatcaaa gccagcggca tgagcaccaa aaagctgctg 300
 ttgattctgt cgcagttcgg ttttattttt gctattgcca ccgtcgcgct cggcgaatgg 360
 gttgcgcca cactgagcca aaaagccgaa aacatcaaag ccgcggccat caacggcaaa 420
 atcagtaccg gcaataccgg cctttggctg aaagaaaaaa acagcattat caatgtgcgc 480
 gaaatgttgc ccgaccatac cctgtctggc attaaaaatct gggcccgcaa cgataaaaaac 540
 gaactggcag aggcagtgga agccgattcc gccgttttga acagcgacgg cagttggcag 600
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 gaagaaaant ggccgatttc cgtcaaacgc aacctgatgg acgtattgct cgtcaaacc 720
 gaccaaagt ccgtcggcga actgaccacc tacatccgcc acctccaaan nnacagccaa 780
 aacaccgaa tctacgccat cgcattgtgg cgcaaattgg tttacccgc cgagcctgg 840
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1071

<210> 56
<211> 356
<212> PRT
<213> Neisseria meningitidis

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Val Tyr Ala Leu Leu Ala Phe Leu Ala Leu Tyr Ser Phe Phe Glu Ile
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Leu Tyr Glu Thr Gly Asn Leu Gly Lys Gly Ser Tyr Gly Ile Trp Glu
35 40 45
Met Xaa Gly Tyr Thr Ala Leu Lys Met Xaa Ala Arg Ala Tyr Glu Leu
50 55 60
Met Pro Leu Ala Val Leu Ile Gly Gly Leu Val Ser Xaa Ser Gln Leu
65 70 75 80
Ala Ala Gly Ser Glu Leu Xaa Val Ile Lys Ala Ser Gly Met Ser Thr
85 90 95
Lys Lys Leu Leu Leu Ile Leu Ser Gln Phe Gly Phe Ile Phe Ala Ile
100 105 110
Ala Thr Val Ala Leu Gly Glu Trp Val Ala Pro Thr Leu Ser Gln Lys
115 120 125
Ala Glu Asn Ile Lys Ala Ala Ala Ile Asn Gly Lys Ile Ser Thr Gly
130 135 140
Asn Thr Gly Leu Trp Leu Lys Glu Lys Asn Ser Ile Ile Asn Val Arg
145 150 155 160
Glu Met Leu Pro Asp His Thr Leu Leu Gly Ile Lys Ile Trp Ala Arg
165 170 175
Asn Asp Lys Asn Glu Leu Ala Glu Ala Val Glu Ala Asp Ser Ala Val
180 185 190
Leu Asn Ser Asp Gly Ser Trp Gln Leu Lys Asn Ile Arg Arg Ser Thr
195 200 205
Leu Gly Glu Asp Lys Val Glu Val Ser Ile Ala Ala Glu Glu Xaa Trp
210 215 220
Pro Ile Ser Val Lys Arg Asn Leu Met Asp Val Leu Leu Val Lys Pro
225 230 235 240
Asp Gln Met Ser Val Gly Glu Leu Thr Thr Tyr Ile Arg His Leu Gln
245 250 255
Xaa Xaa Ser Gln Asn Thr Arg Ile Tyr Ala Ile Ala Trp Trp Arg Lys
260 265 270
Leu Val Tyr Pro Ala Ala Ala Trp Val Met Ala Leu Val Ala Phe Ala
275 280 285
Phe Thr Pro Gln Thr Thr Arg His Gly Asn Met Gly Leu Lys Xaa Phe
290 295 300
Gly Gly Ile Cys Leu Gly Leu Leu Phe His Leu Ala Gly Arg Leu Phe
305 310 315 320

Xaa Phe Thr Ser Gln Leu Tyr Gly Ile Pro Pro Phe Leu Xaa Gly Ala
 325 330 335

Leu Pro Thr Ile Ala Phe Ala Leu Leu Ala Val Trp Leu Ile Arg Lys
 340 345 350

Gln Glu Lys Arg
 355

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 <211> 854
 <212> DNA
 <213> Neisseria meningitidis

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 <211> 284
 <212> PRT
 <213> Neisseria meningitidis

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<400> 58

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20 25 30

Leu Lys Thr Thr Leu Lys Thr Leu Val Cys Ser Leu Val Ser Leu Ser
35 40 45

Met Val Leu Pro Ala His Ala Gln Ile Thr Thr Asp Lys Ser Ala Pro
50 55 60

Lys Asn Gln Gln Val Val Ile Leu Lys Thr Asn Thr Gly Ala Pro Leu
65 70 75 80

Val Asn Ile Gln Thr Pro Asn Gly Arg Gly Leu Ser His Asn Arg Xaa
85 90 95

Tyr Ala Phe Asp Val Asp Asn Lys Gly Ala Val Leu Asn Asn Asp Arg
100 105 110

Asn Asn Asn Pro Phe Val Val Lys Gly Ser Ala Gln Leu Ile Leu Asn
115 120 125

Glu Val Arg Gly Thr Ala Ser Lys Leu Asn Gly Ile Val Thr Val Gly
130 135 140

Gly Gln Lys Ala Asp Val Ile Ile Ala Asn Pro Asn Gly Ile Thr Val
145 150 155 160

Asn Gly Gly Gly Phe Lys Asn Val Gly Arg Gly Ile Leu Thr Thr Gly
165 170 175

Ala Pro Gln Ile Gly Lys Asp Gly Ala Leu Thr Gly Phe Asp Val Val
180 185 190

Lys Ala His Trp Thr Val Xaa Ala Ala Gly Trp Asn Asp Lys Gly Gly
195 200 205

Ala Xaa Tyr Thr Gly Val Leu Ala Arg Ala Val Ala Leu Gln Gly Lys
210 215 220

Xaa Xaa Gly Lys Xaa Leu Ala Val Ser Thr Gly Pro Gln Lys Val Asp
225 230 235 240

Tyr Ala Ser Gly Glu Ile Ser Ala Gly Thr Ala Ala Gly Thr Lys Pro
245 250 255

Thr Ile Ala Leu Asp Thr Ala Ala Leu Gly Gly Met Tyr Ala Asp Ser
260 265 270

Ile Thr Leu Ile Ala Asn Glu Lys Gly Val Gly Val
 275 280

<210> 59
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 <212> DNA
 <213> *Neisseria meningitidis*

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Val	Gly	Gly	Gln	Lys	Ala	Asp	Val	Ile	Ile	Ala	Asn	Pro	Asn	Gly	Ile
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Thr	Val	Asn	Gly	Gly	Gly	Phe	Lys	Asn	Val	Gly	Arg	Gly	Ile	Leu	Thr
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Val	Asp	Tyr	Ala	Ser	Gly	Glu	Ile	Ser	Ala	Gly	Thr	Ala	Ala	Gly	Thr
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 Val Ile Glu Thr Gly Glu Asp Ile Xaa Leu Arg Asn Gly Ala Val Val
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 Xaa Asn Leu Ser Ala Gly Gly Arg Thr Thr Ile Asn Asp Ala Thr Ile
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 Pro Gly Asn Leu Tyr Val His Thr Gly Lys Asp Leu Asn Leu Asn Val
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 Gln Gly Asn Ile Val Ser Asp Gly Leu His Ala Val Ser Ala Asp Gly
 625 630 635 640
 His Val Ser Leu Leu Ala Asn Gly Asn Ala Asp Phe Thr Gly His Asn
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 740 745 750
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Gln Lys Xaa Xaa Xaa Leu Asn Gln Lys Ser Lys Glu Leu Glu Gln Gln 965 970 975		
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 35 40 45
 Ser Thr Ala His Asn Arg Tyr Thr Gly Asn Glu Tyr His Glu Ser Xaa
 50 55 60
 Xaa Ser Gly Val Met Gly Thr Gly Gly Leu Gly Phe Thr Ile Gly Asn
 65 70 75 80
 Arg Lys Thr Thr Asp Asp Thr Asp Arg Thr Asn Ile Val His Thr Gly
 85 90 95

Ser Ile Ile Gly Ser Leu Asn Gly Asp Thr Val Thr Val Ala Gly Asn
 100 105 110
 Arg Tyr Arg Gln Thr Gly Ser Thr Val Ser Ser Pro Glu Gly Arg Asn
 115 120 125
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 Ala Thr Asp Tyr Ala His Thr Gln Glu Gln Lys Gly Leu Thr Val Ala
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 Gln Asn Val Gly Lys Ser Lys Asn Lys Arg Val Asn Ala Met Ala Ala
 180 185 190
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 Phe Ala Pro Ser Ser Ser Ala Gly Gln Gly Gln Asn Tyr Asn Gln Ser
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 Pro Ser Ile Ser Val Ser Ile Xaa Tyr Gly Glu Gln Lys Ser Arg Asn
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 260 265 270
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 275 280 285
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 290 295 300
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 305 310 315 320
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 Val Gly Ser Thr Thr Gly Lys Thr Thr Ile Arg Ser Gly Gly Asp Thr
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 370 375 380
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 385 390 395 400

Lys Gln Gln Asn Gly Asn Val Gln Val Thr Val Gly Tyr Gly Phe Ser
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 Ala Ser Gly Ser Tyr Arg Gln Ser Lys Val Lys Ala Asp His Ala Ser
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 Val Thr Gly Gln Ser Gly Ile Tyr Ala Gly Glu Asp Gly Tyr Gln Ile
 435 440 445
 Lys Val Arg Asp Asn Thr Asp Leu Lys Gly Gly Ile Ile Thr Ser Ser
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 Gln Ser Ala Glu Asp Lys Gly Lys Asn Leu Phe Gln Thr Ala Thr Leu
 465 470 475 480
 Thr Ala Ser Asp Ile Gln Asn His Ser Arg Tyr Glu Gly Arg Ser Phe
 485 490 495
 Gly Ile Gly Gly Ser Phe Asp Leu Asn Gly Gly Trp Asp Gly Thr Val
 500 505 510
 Thr Asp Lys Gln Gly Arg Pro Thr Asp Arg Ile Ser Pro Ala Ala Gly
 515 520 525
 Tyr Gly Ser Asp Gly Asp Ser Lys Asn Ser Thr Thr Arg Ser Gly Val
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 Asn Thr His Asn Ile His Ile Thr Asp Glu Ala Gly Gln Leu Ala Arg
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35 40 45

Gly Gly Ser Gly Gly Ala Val Val Gly Ala Asn Val Asp Trp Asn Asn
50 55 60

Arg Gln Leu His Pro Lys Glu Met Ala Leu Ala Asp Lys Tyr Ala Glu
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Ala Leu Lys Arg Glu Val Glu Lys Arg Glu Gly Arg Lys Ile Ser Ser
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Gln Glu Ala Ala Met Arg Ile Arg Arg Gln Ile Cys Val Gly Trp Thr
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Glu

<210> 67

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ttgraacagc tccaagtcac caaagacgtc aactggaacc aggtacwact ggcgtacgac 180
aaatgggact ataaacagga aggtttaacc ggagccggag cagcgattat tgcgctggct 240
gttaccgtgg ttactgcggg cgcgggagcc ggagccgcac tgggcttaaa cggcgcggcc 300
gcagcggcaa ccgatgccgc attcgcctcg ctggccagcc aggtttccgt atcgctcatc 360
aacaacaaag gcaatatcgg taacaccctg aaagagctgg gcagaagcag cacggtgaaa 420
aatctgatgg ttgccgtcgc taccgcaggc gtagccgaca aaatcgggtgc ttcggcactg 480
aacaatgtca gcgataagca gtggatcaac aacctgaccg tcaacctggc caatgcgggc 540
agtgcgcac tgattaatac cgctgtcaac ggcggcagcc tgaaagacaa tctggaagcg 600
aatatccttg cggcttttgt gaatactgcg catggagaag cagccagtaa aatcaaacag 660
ttggatcagc actacattac ccacaagatt gcccatgcc a tagcgggctg tgcggctgcg 720
gcggcgaata agggcaagtg tcaggatggg gcgatagggt cggctgtggg cgagatagtc 780
ggggaggctt tgacaaacgg caaaaatcct gacactttga cagctaaaga acgcgaacag 840
attttgcat acagcaact ggttgccggt acggtgaagc gtgtgggtcgg cggcgatgta 900
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<210> 68

<211> 319

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 <213> Neisseria meningitidis

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 <223> unknown

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 Lys Tyr Ile Tyr Arg Phe Pro Ile Tyr Cys Pro Xaa Ala Cys Val Ala
 20 25 30
 Glu Asp Thr Pro Tyr Ala Cys Tyr Leu Xaa Gln Leu Gln Val Thr Lys
 35 40 45
 Asp Val Asn Trp Asn Gln Val Xaa Leu Ala Tyr Asp Lys Trp Asp Tyr
 50 55 60
 Lys Gln Glu Gly Leu Thr Gly Ala Gly Ala Ala Ile Ile Ala Leu Ala
 65 70 75 80
 Val Thr Val Val Thr Ala Gly Ala Gly Ala Gly Ala Ala Leu Gly Leu
 85 90 95
 Asn Gly Ala Ala Ala Ala Ala Thr Asp Ala Ala Phe Ala Ser Leu Ala
 100 105 110
 Ser Gln Ala Ser Val Ser Leu Ile Asn Asn Lys Gly Asn Ile Gly Asn
 115 120 125
 Thr Leu Lys Glu Leu Gly Arg Ser Ser Thr Val Lys Asn Leu Met Val
 130 135 140
 Ala Val Ala Thr Ala Gly Val Ala Asp Lys Ile Gly Ala Ser Ala Leu
 145 150 155 160
 Asn Asn Val Ser Asp Lys Gln Trp Ile Asn Asn Leu Thr Val Asn Leu
 165 170 175
 Ala Asn Ala Gly Ser Ala Ala Leu Ile Asn Thr Ala Val Asn Gly Gly
 180 185 190
 Ser Leu Lys Asp Asn Leu Glu Ala Asn Ile Leu Ala Ala Leu Val Asn
 195 200 205

Thr Ala His Gly Glu Ala Ala Ser Lys Ile Lys Gln Leu Asp Gln His
 210 215 220
 Tyr Ile Thr His Lys Ile Ala His Ala Ile Ala Gly Cys Ala Ala Ala
 225 230 235 240
 Ala Ala Asn Lys Gly Lys Cys Gln Asp Gly Ala Ile Gly Ala Ala Val
 245 250 255
 Gly Glu Ile Val Gly Glu Ala Leu Thr Asn Gly Lys Asn Pro Asp Thr
 260 265 270
 Leu Thr Ala Lys Glu Arg Glu Gln Ile Leu Ala Tyr Ser Lys Leu Val
 275 280 285
 Ala Gly Thr Val Ser Gly Val Val Gly Gly Asp Val Asn Ala Ala Ala
 290 295 300
 Asn Ala Ala Glu Val Ala Val Lys Asn Asn Gln Leu Ser Asp Lys
 305 310 315

<210> 69
 <211> 1860
 <212> DNA
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 caactggcgt acgacaaatg ggactataaa caggaaggct taaccggagc cggagcagcg 180
 attattgcgc tggctgttac cgtgggtact gcgggcgcgc gagccggagc cgcactgggc 240
 ttaaacggcg cggccgcgagc ggcaaccgat gccgcattcg cctcgctggc cagccaggct 300
 tccgtatcgc tcatcaacaa caaaggcaat atcggtaaca ccctgaaaga gctgggcaga 360
 agcagcacgg tgaaaaatct gatggttgcc gtcgctaccg caggcgtagc cgacaaaatc 420
 ggtgcttcgg cactgaacaa tgtcagcgat aagcagtga tcaacaacct gaccgtcaac 480
 ctggccaatg cgggcagtg cgcactgatt aataccgctg tcaacggcgc cagcctgaaa 540
 gacaatctgg aagcgaatat ccttgcggct ttggtgaata ctgcgcatgg agaagcagcc 600
 agtaaaatca aacagttgga tcagcactac attaccaca agattgccc tgccatagcg 660
 ggctgtgcgc ctgcggcggc gaataagggc aagtgtcagg atggtgcgat aggtgcggct 720
 gtgggcgaga tagtcgggga ggctttgaca aacggcaaaa atcctgacac ttgacagct 780
 aaagaacgcg aacagatatt ggcatcacgc aaactgggtg ccggtacggt aagcgggtgtg 840
 gtcggcggcg atgtaaatgc ggccggcgaat gcggctgagg tagcgggtgaa aaataatcag 900
 cttagcgaca aagagggtag agaatttgat aacgaaatga ctgcatgcgc caaacagaat 960
 aatcctcaac tgtgcagaaa aaatactgta aaaaagtatc aaaatggtgc tgataaaaga 1020
 cttgctgctt cgattgcaat atgtacggat atatcccgtg gtactgaatg tagaacaatc 1080
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 ggtaaagatg atgaatggta taaattattc agcaaatctt acaccaagc agatttggct 1200
 ttacagtctt atcatttgaa tactgctgct aaatcttggc ttcaatcggg caatacaaaag 1260
 cctttatccg aatggatgtc cgaccaagggt tatacactta tttcaggagt taatcctaga 1320
 ttcatccaa taccaagagg gtttgtaaaa caaaatacac ctattactaa tgtcaaatac 1380
 ccggaaggca tcagtttcga tacaaccta aaaagacatc tggcaaatgc tgatggtttt 1440
 agtcaaaaac agggcattaa aggagcccat aaccgcacca attttatggc agaactaaat 1500
 tcacgaggag gacgcgtaaa atctgaaacc caaactgata ttgaaggcat taccgaatt 1560
 aaatatgaga ttctacact agacaggaca ggtaaacctg atggtggatt taaggaaatt 1620
 tcaagtataa aaactgttta taatcctaaa aaattttctg atgataaaat acttcaaattg 1680
 gctcaaaatg ctgcttcaca aggatattca aaagcctcta aaattgctca aaatgaaaga 1740

actaaatcaa tatcggaag aaaaaatgtc attcaattct cagaaacctt tgacggaatc 1800
aaatttagat catattttga tgtaaataca ggaagaatta caaacattca cccagaataa 1860

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<213> Neisseria meningitidis

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Lys Asp Val Asn Trp Asn Gln Val Gln Leu Ala Tyr Asp Lys Trp Asp
35 40 45
Tyr Lys Gln Glu Gly Leu Thr Gly Ala Gly Ala Ala Ile Ile Ala Leu
50 55 60
Ala Val Thr Val Val Thr Ala Gly Ala Gly Ala Gly Ala Ala Leu Gly
65 70 75 80
Leu Asn Gly Ala Ala Ala Ala Thr Asp Ala Ala Phe Ala Ser Leu
85 90 95
Ala Ser Gln Ala Ser Val Ser Leu Ile Asn Asn Lys Gly Asn Ile Gly
100 105 110
Asn Thr Leu Lys Glu Leu Gly Arg Ser Ser Thr Val Lys Asn Leu Met
115 120 125
Val Ala Val Ala Thr Ala Gly Val Ala Asp Lys Ile Gly Ala Ser Ala
130 135 140
Leu Asn Asn Val Ser Asp Lys Gln Trp Ile Asn Asn Leu Thr Val Asn
145 150 155 160
Leu Ala Asn Ala Gly Ser Ala Ala Leu Ile Asn Thr Ala Val Asn Gly
165 170 175
Gly Ser Leu Lys Asp Asn Leu Glu Ala Asn Ile Leu Ala Ala Leu Val
180 185 190
Asn Thr Ala His Gly Glu Ala Ala Ser Lys Ile Lys Gln Leu Asp Gln
195 200 205
His Tyr Ile Thr His Lys Ile Ala His Ala Ile Ala Gly Cys Ala Ala
210 215 220
Ala Ala Ala Asn Lys Gly Lys Cys Gln Asp Gly Ala Ile Gly Ala Ala
225 230 235 240
Val Gly Glu Ile Val Gly Glu Ala Leu Thr Asn Gly Lys Asn Pro Asp
245 250 255

Thr Leu Thr Ala Lys Glu Arg Glu Gln Ile Leu Ala Tyr Ser Lys Leu
 260 265 270
 Val Ala Gly Thr Val Ser Gly Val Val Gly Gly Asp Val Asn Ala Ala
 275 280 285
 Ala Asn Ala Ala Glu Val Ala Val Lys Asn Asn Gln Leu Ser Asp Lys
 290 295 300
 Glu Gly Arg Glu Phe Asp Asn Glu Met Thr Ala Cys Ala Lys Gln Asn
 305 310 315 320
 Asn Pro Gln Leu Cys Arg Lys Asn Thr Val Lys Lys Tyr Gln Asn Val
 325 330 335
 Ala Asp Lys Arg Leu Ala Ala Ser Ile Ala Ile Cys Thr Asp Ile Ser
 340 345 350
 Arg Ser Thr Glu Cys Arg Thr Ile Arg Lys Gln His Leu Ile Asp Ser
 355 360 365
 Arg Ser Leu His Ser Ser Trp Glu Ala Gly Leu Ile Gly Lys Asp Asp
 370 375 380
 Glu Trp Tyr Lys Leu Phe Ser Lys Ser Tyr Thr Gln Ala Asp Leu Ala
 385 390 395 400
 Leu Gln Ser Tyr His Leu Asn Thr Ala Ala Lys Ser Trp Leu Gln Ser
 405 410 415
 Gly Asn Thr Lys Pro Leu Ser Glu Trp Met Ser Asp Gln Gly Tyr Thr
 420 425 430
 Leu Ile Ser Gly Val Asn Pro Arg Phe Ile Pro Ile Pro Arg Gly Phe
 435 440 445
 Val Lys Gln Asn Thr Pro Ile Thr Asn Val Lys Tyr Pro Glu Gly Ile
 450 455 460
 Ser Phe Asp Thr Asn Leu Lys Arg His Leu Ala Asn Ala Asp Gly Phe
 465 470 475 480
 Ser Gln Lys Gln Gly Ile Lys Gly Ala His Asn Arg Thr Asn Phe Met
 485 490 495
 Ala Glu Leu Asn Ser Arg Gly Gly Arg Val Lys Ser Glu Thr Gln Thr
 500 505 510
 Asp Ile Glu Gly Ile Thr Arg Ile Lys Tyr Glu Ile Pro Thr Leu Asp
 515 520 525
 Arg Thr Gly Lys Pro Asp Gly Gly Phe Lys Glu Ile Ser Ser Ile Lys
 530 535 540
 Thr Val Tyr Asn Pro Lys Lys Phe Ser Asp Asp Lys Ile Leu Gln Met
 545 550 555 560

Ala Gln Asn Ala Ala Ser Gln Gly Tyr Ser Lys Ala Ser Lys Ile Ala
565 570 575

Gln Asn Glu Arg Thr Lys Ser Ile Ser Glu Arg Lys Asn Val Ile Gln
580 585 590

Phe Ser Glu Thr Phe Asp Gly Ile Lys Phe Arg Ser Tyr Phe Asp Val
595 600 605

Asn Thr Gly Arg Ile Thr Asn Ile His Pro Glu
610 615

<210> 71
<211> 1788
<212> DNA
<213> Neisseria meningitidis

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 gccgttaccg tggtcacctc aggcgcagga accggagccg tattgggatt aaacggtgcg 180
 nccgccgccg caaccgatgc agcatctgcc tctttggcca gccaggcttc cgtatcggtc 240
 atcaacaaca aaggcgatgt cggcaaaacc ctgaaagagc tgggcagaag cagcacggtg 300
 aaaaatctgg tggttgccgc cgctaccgca ggcgtagccg acaaaatcgg cgcttcggca 360
 ctgancaatg tcagcgataa gcagtggatc aacaacctga ccgtcaacct agccaatgcg 420
 ggcaagtgcg cactgattaa taccgctgtc aacggcggca gcctgaaaga cantctggaa 480
 gcgaatatcc ttgcggcttt ggtcaatacc gcgcatggag aagcagccag taaaatcaaa 540
 cagttggatc agcaactacat agtccacaag attgcccatg ccatagcggg ctgtgcggca 600

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gcggcggcga ataagggcaa gtgtcaggat ggtgcgatat gtgcggctgt gggcgagata 660
gtcggggagg ctttgacaaa cggcaaaaat cctgacactt tgacagctaa agaacgcgaa 720
cagatTTTtg catacagcaa actggttgcc ggtacggtaa gcggtgtggt cggcggcgat 780
gtaaatgcgg cggcgaatgc ggctgaggta gcggtgaaaa ataatcagct tagcgacnaa 840
gagggtagag aatttgataa cgaaatgact gcatgcgcca aacagaatan tcctcaactg 900
tgcagaaaaa atactgtaaa aaagtatcaa aatgttgctg ataaaagact tgctgcttcg 960
attgcaatat gtacggatat atcccgtagt actgaatgta gaacaatcag aaaacaacat 1020
ttgatcgata gtagaagcct tcattcatct tgggaagcag gtctaattgg taaagatgat 1080
gaatggtata aattattcag caaatcttac acccaagcag atttggtttt acagtcttat 1140
catttgaata ctgctgctaa atcttggctt caatcgggca atacaaagcc tttatccgaa 1200
tggatgtccg accaaggtta tacacttatt tcaggagtta atcctagatt cattccaata 1260
ccaagagggg ttgtaaaaca aaatacacct attactaatg tcaaataccc ggaaggcatc 1320
agtttcgata caaacctana aagacatctg gcaaatgctg atgggttttag tcaagaacag 1380
ggcattaaag gagcccataa ccgcaccaat nttatggcag aactaaattc acgaggagga 1440
ngngtaaaat ctgaaaccca nactgatatt gaaggcatta cccgaattaa atatgagatt 1500
cctacactag acaggacagg taaacctgat ggtggattta aggaaatttc aagtataaaa 1560
actgtttata atcctaaaaa nttttngat gataaaatac ttcaaattgc tcaanatgct 1620
gnttcacaag gatattcaaa agcctctaaa attgctcaaa atgaaagaac taaatcaata 1680
tcggaagaaa aaaatgtcat tcaattctca gaaacctttg acggaatcaa atttagannn 1740
tatntngatg taaatacagg aagaattaca aacattcacc cagaataa 1788

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<210> 72
<211> 595
<212> PRT
<213> Neisseria meningitidis

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 Gln Leu Ala Tyr Asp Arg Trp Asp Tyr Lys Gln Glu Gly Leu Thr Glu
 20 25 30
 Ala Gly Ala Ala Ile Ile Ala Leu Ala Val Thr Val Val Thr Ser Gly
 35 40 45
 Ala Gly Thr Gly Ala Val Leu Gly Leu Asn Gly Ala Xaa Ala Ala Ala
 50 55 60

Thr	Asp	Ala	Ala	Phe	Ala	Ser	Leu	Ala	Ser	Gln	Ala	Ser	Val	Ser	Phe	65	70	75	80
Ile	Asn	Asn	Lys	Gly	Asp	Val	Gly	Lys	Thr	Leu	Lys	Glu	Leu	Gly	Arg	85	90	95	
Ser	Ser	Thr	Val	Lys	Asn	Leu	Val	Val	Ala	Ala	Ala	Thr	Ala	Gly	Val	100	105	110	
Ala	Asp	Lys	Ile	Gly	Ala	Ser	Ala	Leu	Xaa	Asn	Val	Ser	Asp	Lys	Gln	115	120	125	
Trp	Ile	Asn	Asn	Leu	Thr	Val	Asn	Leu	Ala	Asn	Ala	Gly	Ser	Ala	Ala	130	135	140	
Leu	Ile	Asn	Thr	Ala	Val	Asn	Gly	Gly	Ser	Leu	Lys	Asp	Xaa	Leu	Glu	145	150	155	160
Ala	Asn	Ile	Leu	Ala	Ala	Leu	Val	Asn	Thr	Ala	His	Gly	Glu	Ala	Ala	165	170	175	
Ser	Lys	Ile	Lys	Gln	Leu	Asp	Gln	His	Tyr	Ile	Val	His	Lys	Ile	Ala	180	185	190	
His	Ala	Ile	Ala	Gly	Cys	Ala	Ala	Ala	Ala	Ala	Asn	Lys	Gly	Lys	Cys	195	200	205	
Gln	Asp	Gly	Ala	Ile	Gly	Ala	Ala	Val	Gly	Glu	Ile	Val	Gly	Glu	Ala	210	215	220	
Leu	Thr	Asn	Gly	Lys	Asn	Pro	Asp	Thr	Leu	Thr	Ala	Lys	Glu	Arg	Glu	225	230	235	240
Gln	Ile	Leu	Ala	Tyr	Ser	Lys	Leu	Val	Ala	Gly	Thr	Val	Ser	Gly	Val	245	250	255	
Val	Gly	Gly	Asp	Val	Asn	Ala	Ala	Ala	Asn	Ala	Ala	Glu	Val	Ala	Val	260	265	270	
Lys	Asn	Asn	Gln	Leu	Ser	Asp	Xaa	Glu	Gly	Arg	Glu	Phe	Asp	Asn	Glu	275	280	285	
Met	Thr	Ala	Cys	Ala	Lys	Gln	Asn	Xaa	Pro	Gln	Leu	Cys	Arg	Lys	Asn	290	295	300	
Thr	Val	Lys	Lys	Tyr	Gln	Asn	Val	Ala	Asp	Lys	Arg	Leu	Ala	Ala	Ser	305	310	315	320
Ile	Ala	Ile	Cys	Thr	Asp	Ile	Ser	Arg	Ser	Thr	Glu	Cys	Arg	Thr	Ile	325	330	335	
Arg	Lys	Gln	His	Leu	Ile	Asp	Ser	Arg	Ser	Leu	His	Ser	Ser	Trp	Glu	340	345	350	
Ala	Gly	Leu	Ile	Gly	Lys	Asp	Asp	Glu	Trp	Tyr	Lys	Leu	Phe	Ser	Lys	355	360	365	

Ser Tyr Thr Gln Ala Asp Leu Ala Leu Gln Ser Tyr His Leu Asn Thr
 370 375 380
 Ala Ala Lys Ser Trp Leu Gln Ser Gly Asn Thr Lys Pro Leu Ser Glu
 385 390 395 400
 Trp Met Ser Asp Gln Gly Tyr Thr Leu Ile Ser Gly Val Asn Pro Arg
 405 410 415
 Phe Ile Pro Ile Pro Arg Gly Phe Val Lys Gln Asn Thr Pro Ile Thr
 420 425 430
 Asn Val Lys Tyr Pro Glu Gly Ile Ser Phe Asp Thr Asn Leu Xaa Arg
 435 440 445
 His Leu Ala Asn Ala Asp Gly Phe Ser Gln Glu Gln Gly Ile Lys Gly
 450 455 460
 Ala His Asn Arg Thr Asn Xaa Met Ala Glu Leu Asn Ser Arg Gly Gly
 465 470 475 480
 Xaa Val Lys Ser Glu Thr Xaa Thr Asp Ile Glu Gly Ile Thr Arg Ile
 485 490 495
 Lys Tyr Glu Ile Pro Thr Leu Asp Arg Thr Gly Lys Pro Asp Gly Gly
 500 505 510
 Phe Lys Glu Ile Ser Ser Ile Lys Thr Val Tyr Asn Pro Lys Xaa Phe
 515 520 525
 Xaa Asp Asp Lys Ile Leu Gln Met Ala Gln Xaa Ala Xaa Ser Gln Gly
 530 535 540
 Tyr Ser Lys Ala Ser Lys Ile Ala Gln Asn Glu Arg Thr Lys Ser Ile
 545 550 555 560
 Ser Glu Arg Lys Asn Val Ile Gln Phe Ser Glu Thr Phe Asp Gly Ile
 565 570 575
 Lys Phe Arg Xaa Tyr Xaa Asp Val Asn Thr Gly Arg Ile Thr Asn Ile
 580 585 590
 His Pro Glu
 595

<210> 73
 <211> 453
 <212> DNA
 <213> Neisseria meningitidis

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 aaaaatattc aagtagttgc caataataag aatatgggtc tttttgggtt tttggsmrgc 120
 atcatcggcg gttcaaccaa tgccatgtct cccatattgt taatattttt gcttagcgaa 180
 acagaaaata aaaatcgtat cgtaaaatca agcaatctat gctatctttt ggcgaaaatt 240

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gttcaaatat atatgctaag agaccagtat tggttattaa ataagagtga atacgdttta 300
atatttttac tgtccgtatt gtctgttatt ggattgtatg ttggaattcg gttaaggact 360
aagattagcc caaatttttt taaaatgtta atttttattg ttttattggt attggctctg 420
aaaatcgggc attcggggtt aatcaaactt taa 453

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<210> 74
<211> 150
<212> PRT
<213> Neisseria meningitidis

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<222> (39)..(40)
<223> unknown

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<220>
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<222> (99)
<223> unknown

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Cys Ala Lys Ala Lys Asn Ile Gln Val Val Ala Asn Asn Lys Asn Met
          20             25             30

Val Leu Phe Gly Phe Leu Xaa Xaa Ile Ile Gly Gly Ser Thr Asn Ala
  35             40             45

Met Ser Pro Ile Leu Leu Ile Phe Leu Leu Ser Glu Thr Glu Asn Lys
  50             55             60

Asn Arg Ile Val Lys Ser Ser Asn Leu Cys Tyr Leu Leu Ala Lys Ile
  65             70             75             80

Val Gln Ile Tyr Met Leu Arg Asp Gln Tyr Trp Leu Leu Asn Lys Ser
          85             90             95

Glu Tyr Xaa Leu Ile Phe Leu Leu Ser Val Leu Ser Val Ile Gly Leu
  100             105             110

Tyr Val Gly Ile Arg Leu Arg Thr Lys Ile Ser Pro Asn Phe Phe Lys
  115             120             125

Met Leu Ile Phe Ile Val Leu Leu Val Leu Ala Leu Lys Ile Gly His
  130             135             140

Ser Gly Leu Ile Lys Leu
  145             150

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<210> 75
<211> 768
<212> DNA
<213> Neisseria meningitidis

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<400> 75

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gttggttgcc ttggtggcatt accaagcctg ttaatgagct tggtgggttct atgcagcaat 180
aacaaaaagg gtttttggca agagattggt tattatttaa aaacctataa attgcttgct 240
atcggcagcg tcgttggcag cattttgggg gtgaagttgc ttttgatact tccagtgtct 300
tggtgctttt tactgatggc aatcattaca ttgtattatt ctgtcaatgg tattttaaat 360
gtatgtgcaa aagcaaaaaa tattcaagta gttgcccaata ataagaatat ggttcctttt 420
gggtttttgg caggcatcat cggcgggttca accaatgccca tgtctcccat attgttaata 480
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cttttggcga aaattgttca aatataatg ctaagagacc agtattgggt attaaataag 600
agtgaatacg gtttaatat tttactgtcc gtattgtctg ttattggatt gtatgttgga 660
attcggttaa ggactaagat tagcccaaat ttttttaaaa tgtaattttt tattgtttta 720
ttggtattgg ctctgaaaat cgggcattcg gggttaatca aactttaa 768
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<210> 76

<211> 255

<212> PRT

<213> Neisseria meningitidis

<400> 76

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Met Gln Glu Ile Met Gln Ser Ile Val Phe Val Ala Ala Ala Ile Leu
  1             5             10             15

His Gly Ile Thr Gly Met Gly Phe Pro Met Leu Gly Thr Thr Ala Leu
          20             25             30

Ala Phe Ile Met Pro Leu Ser Lys Val Val Ala Leu Val Ala Leu Pro
  35             40             45

Ser Leu Leu Met Ser Leu Leu Val Leu Cys Ser Asn Asn Lys Lys Gly
  50             55             60

Phe Trp Gln Glu Ile Val Tyr Tyr Leu Lys Thr Tyr Lys Leu Leu Ala
  65             70             75             80

Ile Gly Ser Val Val Gly Ser Ile Leu Gly Val Lys Leu Leu Leu Ile
          85             90             95

Leu Pro Val Ser Trp Leu Leu Leu Leu Met Ala Ile Ile Thr Leu Tyr
          100            105            110

Tyr Ser Val Asn Gly Ile Leu Asn Val Cys Ala Lys Ala Lys Asn Ile
          115            120            125

Gln Val Val Ala Asn Asn Lys Asn Met Val Leu Phe Gly Phe Leu Ala
          130            135            140

Gly Ile Ile Gly Gly Ser Thr Asn Ala Met Ser Pro Ile Leu Leu Ile
          145            150            155            160

Phe Leu Leu Ser Glu Thr Glu Asn Lys Asn Arg Ile Val Lys Ser Ser
          165            170            175

Asn Leu Cys Tyr Leu Leu Ala Lys Ile Val Gln Ile Tyr Met Leu Arg
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180	185	190
Asp Gln Tyr Trp Leu Leu Asn Lys Ser Glu Tyr Gly Leu Ile Phe Leu		
195	200	205
Leu Ser Val Leu Ser Val Ile Gly Leu Tyr Val Gly Ile Arg Leu Arg		
210	215	220
Thr Lys Ile Ser Pro Asn Phe Phe Lys Met Leu Ile Phe Ile Val Leu		
225	230	235
Leu Val Leu Ala Leu Lys Ile Gly His Ser Gly Leu Ile Lys Leu		
245	250	255

<210> 77
 <211> 768
 <212> DNA
 <213> Neisseria meningitidis

<400> 77
 atgcaagaaa taatgcaatc tatcggttttt gttgctgccg caatactgca cggaattaca 60
 ggcattgggat ttccgatgct cggtagaacc gcattggcctt ttatcatgcc attgtctaag 120
 gttgttgccct tgggtggcatt accaagcctg ttaatgagct tgggtgttct atgcagcaat 180
 aacaaaaagg gtttttggca agagattggt tattatttaa aaacctataa attgcttgct 240
 atcggcagcg tcgttggcag cattttgggg gtgaagttgc ttttgatact tccagtgtct 300
 tggctgcttt tactgatggc aatcattaca ttgtattatt ctgtcaatgg tattttaaat 360
 gtatgtgcaa aagcaaaaaa tattcaagta gttgccataa ataagaatat ggttcctttt 420
 gggtttttgg caggcatcat cggcggttca accaatgcca tgtctcccat attgttaata 480
 tttttgctta gcgaaacaga gaataaaaat cgtatcgcaa aatcaagcaa tctatgctat 540
 cttttggcaa aaattgttca aatatatatg ctaagagacc agtattgggt attaaataag 600
 agtgaatacg gtttaatat tttactgtcc gtattgtctg ttattggatt gtatgttggg 660
 attcgggttaa ggactaagat tagcccaaat ttttttaaaa tgtaattttt tattgtttta 720
 ttgggtattgg ctctgaaaat cgggtattca ggtttaatca aactttta 768

<210> 78
 <211> 255
 <212> PRT
 <213> Neisseria meningitidis

<400> 78
 Met Gln Glu Ile Met Gln Ser Ile Val Phe Val Ala Ala Ala Ile Leu
 1 5 10 15
 His Gly Ile Thr Gly Met Gly Phe Pro Met Leu Gly Thr Thr Ala Leu
 20 25 30
 Ala Phe Ile Met Pro Leu Ser Lys Val Val Ala Leu Val Ala Leu Pro
 35 40 45
 Ser Leu Leu Met Ser Leu Leu Val Leu Cys Ser Asn Asn Lys Lys Gly
 50 55 60
 Phe Trp Gln Glu Ile Val Tyr Tyr Leu Lys Thr Tyr Lys Leu Leu Ala
 65 70 75 80
 Ile Gly Ser Val Val Gly Ser Ile Leu Gly Val Lys Leu Leu Leu Ile

	85	90	95
Leu Pro Val Ser Trp Leu Leu Leu Leu Met Ala Ile Ile Thr Leu Tyr	100	105	110
Tyr Ser Val Asn Gly Ile Leu Asn Val Cys Ala Lys Ala Lys Asn Ile	115	120	125
Gln Val Val Ala Asn Asn Lys Asn Met Val Leu Phe Gly Phe Leu Ala	130	135	140
Gly Ile Ile Gly Gly Ser Thr Asn Ala Met Ser Pro Ile Leu Leu Ile	145	150	155
Phe Leu Leu Ser Glu Thr Glu Asn Lys Asn Arg Ile Ala Lys Ser Ser	165	170	175
Asn Leu Cys Tyr Leu Leu Ala Lys Ile Val Gln Ile Tyr Met Leu Arg	180	185	190
Asp Gln Tyr Trp Leu Leu Asn Lys Ser Glu Tyr Gly Leu Ile Phe Leu	195	200	205
Leu Ser Val Leu Ser Val Ile Gly Leu Tyr Val Gly Ile Arg Leu Arg	210	215	220
Thr Lys Ile Ser Pro Asn Phe Phe Lys Met Leu Ile Phe Ile Val Leu	225	230	235
Leu Val Leu Ala Leu Lys Ile Gly Tyr Ser Gly Leu Ile Lys Leu	245	250	255

<210> 79
 <211> 516
 <212> DNA
 <213> Neisseria meningitidis

<400> 79
 atgagacata tgaaaataca aaattatttta ctagtatttta tagttttaca tatagccttg 60
 atagtaatta atatagtgtt tgggtattttt gtttttctat ttgatttttt tgcggtttttg 120
 ttttttgcaa acgtctttct tgctgtaaat ttattatttt tagaaaaaaa cataaaaaaac 180
 aaattattgt ttttattgcc gatttctatt attatatgga tggtaattca tattagtatg 240
 ataaatataa aattttataa atttgagcat caaataaagg aacaaaatat atcctcgatt 300
 actggggtga taaaaccaca tgatagttat aattatgttt atgactcaaa tggatatgct 360
 aaattaaaag ataatcatag atatggtagg gtaattagag aaacacctta tattgatgta 420
 gttgcatctg atgttaaaaa taaatccata agattaagct tggtttgtgg tattcattca 480
 tatgctccat gtgccaattt tataaaattt gtcagg 516

<210> 80
 <211> 172
 <212> PRT
 <213> Neisseria meningitidis

<400> 80
 Met Arg His Met Lys Ile Gln Asn Tyr Leu Leu Val Phe Ile Val Leu

1	5	10	15
His Ile Ala Leu Ile Val Ile Asn Ile Val Phe Gly Tyr Phe Val Phe	20	25	30
Leu Phe Asp Phe Phe Ala Phe Leu Phe Phe Ala Asn Val Phe Leu Ala	35	40	45
Val Asn Leu Leu Phe Leu Glu Lys Asn Ile Lys Asn Lys Leu Leu Phe	50	55	60
Leu Leu Pro Ile Ser Ile Ile Ile Trp Met Val Ile His Ile Ser Met	65	70	75
Ile Asn Ile Lys Phe Tyr Lys Phe Glu His Gln Ile Lys Glu Gln Asn	85	90	95
Ile Ser Ser Ile Thr Gly Val Ile Lys Pro His Asp Ser Tyr Asn Tyr	100	105	110
Val Tyr Asp Ser Asn Gly Tyr Ala Lys Leu Lys Asp Asn His Arg Tyr	115	120	125
Gly Arg Val Ile Arg Glu Thr Pro Tyr Ile Asp Val Val Ala Ser Asp	130	135	140
Val Lys Asn Lys Ser Ile Arg Leu Ser Leu Val Cys Gly Ile His Ser	145	150	155
Tyr Ala Pro Cys Ala Asn Phe Ile Lys Phe Val Arg	165	170	

<210> 81
 <211> 729
 <212> DNA
 <213> Neisseria meningitidis

<400> 81
 atgagacata tgaaaaataa aaattatttta ctagtatttta tagttttaca tatagccttg 60
 atagtaatta atatagtgtt tgggtattttt gtttttctat ttgattttttt tgcgtttttt 120
 ttttttgcaa acgtcttttct tgctgtaaat ttattatttt tagaaaaaaa cataaaaaaac 180
 aaattattgt ttttattgcc gatttctatt attatatgga tggtaattca tattagtatg 240
 ataaatataa aattttataa atttgagcat caaataaagg aacaaaatat atcctcgatt 300
 actgggggtga taaaaccaca tgatagttat aattatgttt atgactcaaa tggatatgct 360
 aaattaaaag ataatcatag atatggtagg gtaattagag aaacacctta tattgatgta 420
 gttgcatctg atgttaaaaa taaatccata agattaagct tggtttgtgg tattcattca 480
 tatgctccat gtgccaattt tataaaattt gcaaaaaaac ctgttaaaat ttattttttat 540
 aatcaacctc aaggagattt tatagataat gtaatatattg aaattaatga tggaaacaaa 600
 agtttgtact tgttagataa gtataaaaca ttttttctta ttgaaaacag tgtttgtatc 660
 gtattaatta ttttatattt aaaatttaaat ttgcttttat ataggactta cttcaatgag 720
 ttggaatag 729

<210> 82
 <211> 242
 <212> PRT

<213> Neisseria meningitidis

<400> 82

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Met Arg His Met Lys Asn Lys Asn Tyr Leu Leu Val Phe Ile Val Leu
 1           5           10           15

His Ile Ala Leu Ile Val Ile Asn Ile Val Phe Gly Tyr Phe Val Phe
      20           25           30

Leu Phe Asp Phe Phe Ala Phe Leu Phe Phe Ala Asn Val Phe Leu Ala
      35           40           45

Val Asn Leu Leu Phe Leu Glu Lys Asn Ile Lys Asn Lys Leu Leu Phe
      50           55           60

Leu Leu Pro Ile Ser Ile Ile Ile Trp Met Val Ile His Ile Ser Met
      65           70           75           80

Ile Asn Ile Lys Phe Tyr Lys Phe Glu His Gln Ile Lys Glu Gln Asn
      85           90           95

Ile Ser Ser Ile Thr Gly Val Ile Lys Pro His Asp Ser Tyr Asn Tyr
      100          105          110

Val Tyr Asp Ser Asn Gly Tyr Ala Lys Leu Lys Asp Asn His Arg Tyr
      115          120          125

Gly Arg Val Ile Arg Glu Thr Pro Tyr Ile Asp Val Val Ala Ser Asp
      130          135          140

Val Lys Asn Lys Ser Ile Arg Leu Ser Leu Val Cys Gly Ile His Ser
      145          150          155          160

Tyr Ala Pro Cys Ala Asn Phe Ile Lys Phe Ala Lys Lys Pro Val Lys
      165          170          175

Ile Tyr Phe Tyr Asn Gln Pro Gln Gly Asp Phe Ile Asp Asn Val Ile
      180          185          190

Phe Glu Ile Asn Asp Gly Asn Lys Ser Leu Tyr Leu Leu Asp Lys Tyr
      195          200          205

Lys Thr Phe Phe Leu Ile Glu Asn Ser Val Cys Ile Val Leu Ile Ile
      210          215          220

Leu Tyr Leu Lys Phe Asn Leu Leu Leu Tyr Arg Thr Tyr Phe Asn Glu
      225          230          235          240

Leu Glu
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<210> 83

<211> 729

<212> DNA

<213> Neisseria meningitidis


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<400> 83
atgagacata tgaaaaataa aaattattta ctagtattta tagttttaca tataaccttg 60
atagtaatta atatagtgtt tgggtatttt gtttttctat ttgatttttt tgcgtttttg 120
ttttttgcaa acgtctttct tgctgtaaat ttattatttt tagaaaaaaa cataaaaaaac 180
aaattattgt ttttattgcc gattttctatt attatatgga tggtaattca tattagtatg 240
ataaatataa aattttataa atttgagcat caaataaagg aacaaaatat atcctcgatt 300
actggggtga taaaaccaca tgatagtatt aattatgttt atgactcaaa tggatatgct 360
aaattaaaag ataatcatag atatggtagg gtaattagag aaacacctta tattgatgta 420
gttgcatctg atgttaaaaa taaatccata agattaagct tggtttgtgg tattcattca 480
tatgctccat gtgccaattt tataaaattt gcaaaaaaac ctgttaaaat ttatttttat 540
aatcaacctc aaggagattt tatagataat gtaatatattg aaattaatga tggaaaaaaa 600
agtttg tact tgtagataa gtataaaaca ttttttctta ttgaaaacag tgtttgtatc 660
gtattaatta ttttatattt aaaatttaat ttgcttttat ataggactta cttcaatgag 720
ttggaatag 729

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<210> 84
<211> 242
<212> PRT
<213> Neisseria meningitidis

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<400> 84
Met Arg His Met Lys Asn Lys Asn Tyr Leu Leu Val Phe Ile Val Leu
  1             5             10             15

His Ile Thr Leu Ile Val Ile Asn Ile Val Phe Gly Tyr Phe Val Phe
      20             25             30

Leu Phe Asp Phe Phe Ala Phe Leu Phe Phe Ala Asn Val Phe Leu Ala
      35             40             45

Val Asn Leu Leu Phe Leu Glu Lys Asn Ile Lys Asn Lys Leu Leu Phe
      50             55             60

Leu Leu Pro Ile Ser Ile Ile Ile Trp Met Val Ile His Ile Ser Met
      65             70             75             80

Ile Asn Ile Lys Phe Tyr Lys Phe Glu His Gln Ile Lys Glu Gln Asn
      85             90             95

Ile Ser Ser Ile Thr Gly Val Ile Lys Pro His Asp Ser Tyr Asn Tyr
      100            105            110

Val Tyr Asp Ser Asn Gly Tyr Ala Lys Leu Lys Asp Asn His Arg Tyr
      115            120            125

Gly Arg Val Ile Arg Glu Thr Pro Tyr Ile Asp Val Val Ala Ser Asp
      130            135            140

Val Lys Asn Lys Ser Ile Arg Leu Ser Leu Val Cys Gly Ile His Ser
      145            150            155            160

Tyr Ala Pro Cys Ala Asn Phe Ile Lys Phe Ala Lys Lys Pro Val Lys
      165            170            175

Ile Tyr Phe Tyr Asn Gln Pro Gln Gly Asp Phe Ile Asp Asn Val Ile
      180            185            190

```

Phe Glu Ile Asn Asp Gly Lys Lys Ser Leu Tyr Leu Leu Asp Lys Tyr
 195 200 205

Lys Thr Phe Phe Leu Ile Glu Asn Ser Val Cys Ile Val Leu Ile Ile
 210 215 220

Leu Tyr Leu Lys Phe Asn Leu Leu Leu Tyr Arg Thr Tyr Phe Asn Glu
 225 230 235 240

Leu Glu

<210> 85
 <211> 552
 <212> DNA
 <213> Neisseria meningitidis
 <400> 85
 accccaaca gcgtgaccgt cttgccgtct ttcggcggat tcgggcgtac cggcgcgacc 60
 atcaatgcag caggcggggt cggcatgact gccttttcga caaccttaat ttccgtagcc 120
 gagggcgcgg ttgtagagct gcaggccgtg agagccaaag ccgtcaatgc aaccgccgct 180
 tgcattttta cggctcttgag taaggacatt ttcgatttcc tttttatttt ccgttttcag 240
 acggctgact tccgcctgta ttttcgccaa agccatgccg acagcgtgcg ccttgacttc 300
 atatttaaaa gcttcgcgcg gtgccagttc cagttcgcgc gcatagtttt gagccgacaa 360
 cagcagggct tgcgccttgt cgcgctccat cttgtcgatg accgcctgca gcttcgcaaa 420
 tgccgacttg tagccttgat ggtgcgacac agccaagccc gtgccgacaa gcgcgataat 480
 ggcaatcggg tgccagtaat tcgccagcag tttcacgaga ttcattctcg acctcctgac 540
 gcttcacgct ga 552

<210> 86
 <211> 183
 <212> PRT
 <213> Neisseria meningitidis
 <400> 86
 Thr Pro Asn Ser Val Thr Val Leu Pro Ser Phe Gly Gly Phe Gly Arg
 1 5 10 15
 Thr Gly Ala Thr Ile Asn Ala Ala Gly Gly Val Gly Met Thr Ala Phe
 20 25 30
 Ser Thr Thr Leu Ile Ser Val Ala Glu Gly Ala Val Val Glu Leu Gln
 35 40 45
 Ala Val Arg Ala Lys Ala Val Asn Ala Thr Ala Ala Cys Ile Phe Thr
 50 55 60
 Val Leu Ser Lys Asp Ile Phe Asp Phe Leu Phe Ile Phe Arg Phe Gln
 65 70 75 80
 Thr Ala Asp Phe Arg Leu Tyr Phe Arg Gln Ser His Ala Asp Ser Val
 85 90 95
 Arg Leu Asp Phe Ile Phe Lys Ser Phe Arg Ala Cys Gln Phe Gln Phe
 100 105 110

Ala Arg Ile Val Leu Ser Arg Gln Gln Gln Gly Leu Arg Leu Val Ala
115 120 125

Leu His Leu Val Asp Asp Arg Leu Gln Leu Arg Lys Cys Arg Leu Val
130 135 140

Ala Leu Met Val Arg His Ser Gln Ala Arg Ala Asp Lys Arg Asp Asn
145 150 155 160

Gly Asn Arg Leu Pro Val Ile Arg Gln Gln Phe His Glu Ile His Ser
165 170 175

Arg Pro Pro Asp Ala Ser Arg
180

<210> 87
<211> 468
<212> DNA
<213> Neisseria meningitidis

<400> 87
atgactgcct tttcgacaac ctttaatttcc gtagccgagg gcgcggttgt agagctgcag 60
gccgtgagag ccaaagccgt caatgcaacc gccgcttgca tttttacggt cttgagtaag 120
gacatttttcg atttcctttt tattttccgt tttcagacgg ctgacttccg cctgtttttt 180
cgccaaagcc atgccgacag cgtgcgcctt gacttcatat tttttagctt ccgcgcgtgc 240
cagttccagt tcgcgcgcat agttttgagc cgacaacagc agggcttgcg ccttgtcgcg 300
ctccatcttg tcgatgaccg cctgctgctt cgcaaagtgc gacttgtagc cttgatggtg 360
cgacacagcc aagcccgtgc cgacaagcgc gataatggca atcggttgcc agttattcgc 420
cagcagtttc acgagattca ttctcgacct cctgacgctt cagcgtga 468

<210> 88
<211> 155
<212> PRT
<213> Neisseria meningitidis

<400> 88
Met Thr Ala Phe Ser Thr Thr Leu Ile Ser Val Ala Glu Gly Ala Val
1 5 10 15

Val Glu Leu Gln Ala Val Arg Ala Lys Ala Val Asn Ala Thr Ala Ala
20 25 30

Cys Ile Phe Thr Val Leu Ser Lys Asp Ile Phe Asp Phe Leu Phe Ile
35 40 45

Phe Arg Phe Gln Thr Ala Asp Phe Arg Leu Phe Phe Arg Gln Ser His
50 55 60

Ala Asp Ser Val Arg Leu Asp Phe Ile Phe Phe Ser Phe Arg Ala Cys
65 70 75 80

Gln Phe Gln Phe Ala Arg Ile Val Leu Ser Arg Gln Gln Gln Gly Leu
85 90 95

Arg Leu Val Ala Leu His Leu Val Asp Asp Arg Leu Leu Leu Arg Lys

	100		105		110										
Cys	Arg	Leu	Val	Ala	Leu	Met	Val	Arg	His	Ser	Gln	Ala	Arg	Ala	Asp
	115						120				125				
Lys	Arg	Asp	Asn	Gly	Asn	Arg	Leu	Pro	Val	Ile	Arg	Gln	Gln	Phe	His
	130					135					140				
Glu	Ile	His	Ser	Arg	Pro	Pro	Asp	Ala	Ser	Arg					
145					150					155					

<210> 89
 <211> 462
 <212> DNA
 <213> Neisseria meningitidis

<400> 89
 atgaccgcct tttcgacaac cttaattttcc gtagccgagg gcgcgcttgt agagctgcaa 60
 gccgtgatgg ccaaagccgt caatacaacc gccgcctgca tttttacggt cttgagtaag 120
 gacatttttcg atttcctttt tattttccgt tttcagacgg ctgacttccg cctgtttttt 180
 cgccaaagcc atgccgacgg cgtgcgcctt gacttcatat ttttagctt ccgcacgcgc 240
 ctgttccagt tcgcgggctt agttttgagc cgacaacagc agggcttgcg ccttgtcgcg 300
 cttcatittt tcaatgaccg cctgctgctt cgcaaaagcc gacttgtagc cttgatggtg 360
 cgacaccgcc aaaccgctgc cgacaagcgc gatgatggca atcggttgcc agttattcgc 420
 cagcagtttc acgagattca ttctcgacct cctgacgttt ga 462

<210> 90
 <211> 153
 <212> PRT
 <213> Neisseria meningitidis

<400> 90
 Met Thr Ala Phe Ser Thr Thr Leu Ile Ser Val Ala Glu Gly Ala Leu
 1 5 10 15
 Val Glu Leu Gln Ala Val Met Ala Lys Ala Val Asn Thr Thr Ala Ala
 20 25 30
 Cys Ile Phe Thr Val Leu Ser Lys Asp Ile Phe Asp Phe Leu Phe Ile
 35 40 45
 Phe Arg Phe Gln Thr Ala Asp Phe Arg Leu Phe Phe Arg Gln Ser His
 50 55 60
 Ala Asp Gly Val Arg Leu Asp Phe Ile Phe Phe Ser Phe Arg Thr Arg
 65 70 75 80
 Leu Phe Gln Phe Ala Gly Val Val Leu Ser Arg Gln Gln Gln Gly Leu
 85 90 95
 Arg Leu Val Ala Leu His Phe Leu Asn Asp Arg Leu Leu Leu Arg Lys
 100 105 110
 Ser Arg Leu Val Ala Leu Met Val Arg His Arg Gln Thr Arg Ala Asp
 115 120 125

Lys Arg Asp Asp Gly Asn Arg Leu Pro Val Ile Arg Gln Gln Phe His
 130 135 140

Glu Ile His Ser Arg Pro Pro Asp Val
 145 150

<210> 91
 <211> 592
 <212> PRT
 <213> Neisseria meningitidis

<400> 91
 Met Asn Lys Ile Tyr Arg Ile Ile Trp Asn Ser Ala Leu Asn Ala Trp
 1 5 10 15

Val Ala Val Ser Glu Leu Thr Arg Asn His Thr Lys Arg Ala Ser Ala
 20 25 30

Thr Val Lys Thr Ala Val Leu Ala Thr Leu Leu Phe Ala Thr Val Gln
 35 40 45

Ala Asn Ala Thr Asp Glu Asp Glu Glu Glu Glu Leu Glu Ser Val Gln
 50 55 60

Arg Ser Val Val Gly Ser Ile Gln Ala Ser Met Glu Gly Ser Gly Glu
 65 70 75 80

Leu Glu Thr Ile Ser Leu Ser Met Thr Asn Asp Ser Lys Glu Phe Val
 85 90 95

Asp Pro Tyr Ile Val Val Thr Leu Lys Ala Gly Asp Asn Leu Lys Ile
 100 105 110

Lys Gln Asn Thr Asn Glu Asn Thr Asn Ala Ser Ser Phe Thr Tyr Ser
 115 120 125

Leu Lys Lys Asp Leu Thr Gly Leu Ile Asn Val Glu Thr Glu Lys Leu
 130 135 140

Ser Phe Gly Ala Asn Gly Lys Lys Val Asn Ile Ile Ser Asp Thr Lys
 145 150 155 160

Gly Leu Asn Phe Ala Lys Glu Thr Ala Gly Thr Asn Gly Asp Thr Thr
 165 170 175

Val His Leu Asn Gly Ile Gly Ser Thr Leu Thr Asp Thr Leu Ala Gly
 180 185 190

Ser Ser Ala Ser His Val Asp Ala Gly Asn Gln Ser Thr His Tyr Thr
 195 200 205

Arg Ala Ala Ser Ile Lys Asp Val Leu Asn Ala Gly Trp Asn Ile Lys
 210 215 220

Gly Val Lys Thr Gly Ser Thr Thr Gly Gln Ser Glu Asn Val Asp Phe

225		230		235		240
Val Arg Thr Tyr	Asp Thr Val Glu Phe Leu Ser Ala Asp Thr Lys Thr					
	245			250		255
Thr Thr Val Asn Val Glu Ser Lys Asp Asn Gly Lys Arg Thr Glu Val						
	260			265		270
Lys Ile Gly Ala Lys Thr Ser Val Ile Lys Glu Lys Asp Gly Lys Leu						
	275			280		285
Val Thr Gly Lys Gly Lys Gly Glu Asn Gly Ser Ser Thr Asp Glu Gly						
	290			295		300
Glu Gly Leu Val Thr Ala Lys Glu Val Ile Asp Ala Val Asn Lys Ala						
305		310		315		320
Gly Trp Arg Met Lys Thr Thr Thr Ala Asn Gly Gln Thr Gly Gln Ala						
	325			330		335
Asp Lys Phe Glu Thr Val Thr Ser Gly Thr Asn Val Thr Phe Ala Ser						
	340			345		350
Gly Lys Gly Thr Thr Ala Thr Val Ser Lys Asp Asp Gln Gly Asn Ile						
	355			360		365
Thr Val Met Tyr Asp Val Asn Val Gly Asp Ala Leu Asn Val Asn Gln						
	370			375		380
Leu Gln Asn Ser Gly Trp Asn Leu Asp Ser Lys Ala Val Ala Gly Ser						
385		390		395		400
Ser Gly Lys Val Ile Ser Gly Asn Val Ser Pro Ser Lys Gly Lys Met						
	405			410		415
Asp Glu Thr Val Asn Ile Asn Ala Gly Asn Asn Ile Glu Ile Ser Arg						
	420			425		430
Asn Gly Lys Asn Ile Asp Ile Ala Thr Ser Met Ala Pro Gln Phe Ser						
	435			440		445
Ser Val Ser Leu Gly Ala Gly Ala Asp Ala Pro Thr Leu Ser Val Asp						
	450			455		460
Asp Glu Gly Ala Leu Asn Val Gly Ser Lys Asp Ala Asn Lys Pro Val						
465		470		475		480
Arg Ile Thr Asn Val Ala Pro Gly Val Lys Glu Gly Asp Val Thr Asn						
	485			490		495
Val Ala Gln Leu Lys Gly Val Ala Gln Asn Leu Asn Asn Arg Ile Asp						
	500			505		510
Asn Val Asp Gly Asn Ala Arg Ala Gly Ile Ala Gln Ala Ile Ala Thr						
	515			520		525
Ala Gly Leu Val Gln Ala Tyr Leu Pro Gly Lys Ser Met Met Ala Ile						
	530			535		540

Gly Gly Gly Thr Tyr Arg Gly Glu Ala Gly Tyr Ala Ile Gly Tyr Ser
545 550 555 560

Ser Ile Ser Asp Gly Gly Asn Trp Ile Ile Lys Gly Thr Ala Ser Gly
565 570 575

Asn Ser Arg Gly His Phe Gly Ala Ser Ala Ser Val Gly Tyr Gln Trp
580 585 590

<210> 92
<211> 594
<212> PRT
<213> Neisseria meningitidis

<400> 92
Met Asn Lys Ile Tyr Arg Ile Ile Trp Asn Ser Ala Leu Asn Ala Trp
1 5 10 15

Val Val Val Ser Glu Leu Thr Arg Asn His Thr Lys Arg Ala Ser Ala
20 25 30

Thr Val Ala Thr Ala Val Leu Ala Thr Leu Leu Phe Ala Thr Val Gln
35 40 45

Ala Asn Ala Thr Asp Asp Asp Asp Leu Tyr Leu Glu Pro Val Gln Arg
50 55 60

Thr Ala Val Val Leu Ser Phe Arg Ser Asp Lys Glu Gly Thr Gly Glu
65 70 75 80

Lys Glu Gly Thr Glu Asp Ser Asn Trp Ala Val Tyr Phe Asp Glu Lys
85 90 95

Arg Val Leu Lys Ala Gly Ala Ile Thr Leu Lys Ala Gly Asp Asn Leu
100 105 110

Lys Ile Lys Gln Asn Thr Asn Glu Asn Thr Asn Asp Ser Ser Phe Thr
115 120 125

Tyr Ser Leu Lys Lys Asp Leu Thr Asp Leu Thr Ser Val Glu Thr Glu
130 135 140

Lys Leu Ser Phe Gly Ala Asn Gly Asn Lys Val Asn Ile Thr Ser Asp
145 150 155 160

Thr Lys Gly Leu Asn Phe Ala Lys Glu Thr Ala Gly Thr Asn Gly Asp
165 170 175

Pro Thr Val His Leu Asn Gly Ile Gly Ser Thr Leu Thr Asp Thr Leu
180 185 190

Leu Asn Thr Gly Ala Thr Thr Asn Val Thr Asn Asp Asn Val Thr Asp

195					200					205					
Asp	Glu	Lys	Lys	Arg	Ala	Ala	Ser	Val	Lys	Asp	Val	Leu	Asn	Ala	Gly
210					215					220					
Trp	Asn	Ile	Lys	Gly	Val	Lys	Pro	Gly	Thr	Thr	Ala	Ser	Asp	Asn	Val
225					230					235					240
Asp	Phe	Val	Arg	Thr	Tyr	Asp	Thr	Val	Glu	Phe	Leu	Ser	Ala	Asp	Thr
				245					250					255	
Lys	Thr	Thr	Thr	Val	Asn	Val	Glu	Ser	Lys	Asp	Asn	Gly	Lys	Lys	Thr
			260					265					270		
Glu	Val	Lys	Ile	Gly	Ala	Lys	Thr	Ser	Val	Ile	Lys	Glu	Lys	Asp	Gly
		275					280					285			
Lys	Leu	Val	Thr	Gly	Lys	Gly	Lys	Asp	Glu	Asn	Gly	Ser	Ser	Thr	Asp
	290					295					300				
Glu	Gly	Glu	Gly	Leu	Val	Thr	Ala	Lys	Glu	Val	Ile	Asp	Ala	Val	Asn
305				310					315						320
Lys	Ala	Gly	Trp	Arg	Met	Lys	Thr	Thr	Thr	Ala	Asn	Gly	Gln	Thr	Gly
				325					330					335	
Gln	Ala	Asp	Lys	Phe	Glu	Thr	Val	Thr	Ser	Gly	Thr	Asn	Val	Thr	Phe
			340					345					350		
Ala	Ser	Gly	Lys	Gly	Thr	Thr	Ala	Thr	Val	Ser	Lys	Asp	Asp	Gln	Gly
		355					360					365			
Asn	Ile	Thr	Val	Lys	Tyr	Asp	Val	Asn	Val	Gly	Asp	Ala	Leu	Asn	Val
	370					375					380				
Asn	Gln	Leu	Gln	Asn	Ser	Gly	Trp	Asn	Leu	Asp	Ser	Lys	Ala	Val	Ala
385				390					395						400
Gly	Ser	Ser	Gly	Lys	Val	Ile	Ser	Gly	Asn	Val	Ser	Pro	Ser	Lys	Gly
			405					410						415	
Lys	Met	Asp	Glu	Thr	Val	Asn	Ile	Asn	Ala	Gly	Asn	Asn	Ile	Glu	Ile
		420						425					430		
Thr	Arg	Asn	Gly	Lys	Asn	Ile	Asp	Ile	Ala	Thr	Ser	Met	Ala	Pro	Gln
		435					440					445			
Phe	Ser	Ser	Val	Ser	Leu	Gly	Ala	Gly	Ala	Asp	Ala	Pro	Thr	Leu	Ser
450						455					460				
Val	Asp	Asp	Glu	Gly	Ala	Leu	Asn	Val	Gly	Ser	Lys	Asp	Thr	Asn	Lys
465				470					475						480
Pro	Val	Arg	Ile	Thr	Asn	Val	Ala	Pro	Gly	Val	Lys	Glu	Gly	Asp	Val
			485					490						495	
Thr	Asn	Val	Ala	Gln	Leu	Lys	Gly	Val	Ala	Gln	Asn	Leu	Asn	Asn	Arg

500	505	510
Ile Asp Asn Val Asp Gly Asn Ala Arg Ala Gly Ile Ala Gln Ala Ile		
515	520	525
Ala Thr Ala Gly Leu Val Gln Ala Tyr Leu Pro Gly Lys Ser Met Met		
530	535	540
Ala Ile Gly Gly Asp Thr Tyr Arg Gly Glu Ala Gly Tyr Ala Ile Gly		
545	550	555
Tyr Ser Ser Ile Ser Asp Gly Gly Asn Trp Ile Ile Lys Gly Thr Ala		
565	570	575
Ser Gly Asn Ser Arg Gly His Phe Gly Ala Ser Ala Ser Val Gly Tyr		
580	585	590

Gln Trp

<210> 93
 <211> 594
 <212> PRT
 <213> Neisseria meningitidis

<400> 93
Met Asn Lys Ile Tyr Arg Ile Ile Trp Asn Ser Ala Leu Asn Ala Trp
1 5 10 15
Val Ala Val Ser Glu Leu Thr Arg Asn His Thr Lys Arg Ala Ser Ala
20 25 30
Thr Val Ala Thr Ala Val Leu Ala Thr Leu Leu Phe Ala Thr Val Gln
35 40 45
Ala Ser Thr Thr Asp Asp Asp Asp Leu Tyr Leu Glu Pro Val Gln Arg
50 55 60
Thr Ala Pro Val Leu Ser Phe His Ala Asp Ser Glu Gly Thr Gly Glu
65 70 75 80
Lys Glu Val Thr Glu Asp Ser Asn Trp Gly Val Tyr Phe Asp Lys Lys
85 90 95
Gly Val Leu Thr Ala Gly Thr Ile Thr Leu Lys Ala Gly Asp Asn Leu
100 105 110
Lys Ile Lys Gln Asn Thr Asp Glu Asn Thr Asn Ala Ser Ser Phe Thr
115 120 125
Tyr Ser Leu Lys Lys Asp Leu Thr Asp Leu Thr Ser Val Glu Thr Glu
130 135 140
Lys Leu Ser Phe Gly Ala Asn Gly Lys Lys Val Asn Ile Thr Ser Asp
145 150 155 160

Thr Lys Gly Leu Asn Phe Ala Lys Glu Thr Ala Gly Thr Asn Gly Asp
 165 170 175
 Thr Thr Val His Leu Asn Gly Ile Gly Ser Thr Leu Thr Asp Thr Leu
 180 185 190
 Leu Asn Thr Gly Ala Thr Thr Asn Val Thr Asn Asp Asn Val Thr Asp
 195 200 205
 Asp Glu Lys Lys Arg Ala Ala Ser Val Lys Asp Val Leu Asn Ala Gly
 210 215 220
 Trp Asn Ile Lys Gly Val Lys Pro Gly Thr Thr Ala Ser Asp Asn Val
 225 230 235 240
 Asp Phe Val Arg Thr Tyr Asp Thr Val Glu Phe Leu Ser Ala Asp Thr
 245 250 255
 Lys Thr Thr Thr Val Asn Val Glu Ser Lys Asp Asn Gly Lys Lys Thr
 260 265 270
 Glu Val Lys Ile Gly Ala Lys Thr Ser Val Ile Lys Glu Lys Asp Gly
 275 280 285
 Lys Leu Val Thr Gly Lys Asp Lys Gly Glu Asn Gly Ser Ser Thr Asp
 290 295 300
 Glu Gly Glu Gly Leu Val Thr Ala Lys Glu Val Ile Asp Ala Val Asn
 305 310 315 320
 Lys Ala Gly Trp Arg Met Lys Thr Thr Thr Ala Asn Gly Gln Thr Gly
 325 330 335
 Gln Ala Asp Lys Phe Glu Thr Val Thr Ser Gly Thr Lys Val Thr Phe
 340 345 350
 Ala Ser Gly Asn Gly Thr Thr Ala Thr Val Ser Lys Asp Asp Gln Gly
 355 360 365
 Asn Ile Thr Val Lys Tyr Asp Val Asn Val Gly Asp Ala Leu Asn Val
 370 375 380
 Asn Gln Leu Gln Asn Ser Gly Trp Asn Leu Asp Ser Lys Ala Val Ala
 385 390 395 400
 Gly Ser Ser Gly Lys Val Ile Ser Gly Asn Val Ser Pro Ser Lys Gly
 405 410 415
 Lys Met Asp Glu Thr Val Asn Ile Asn Ala Gly Asn Asn Ile Glu Ile
 420 425 430
 Thr Arg Asn Gly Lys Asn Ile Asp Ile Ala Thr Ser Met Thr Pro Gln
 435 440 445
 Phe Ser Ser Val Ser Leu Gly Ala Gly Ala Asp Ala Pro Thr Leu Ser
 450 455 460

Val Asp Asp Glu Gly Ala Leu Asn Val Gly Ser Lys Asp Ala Asn Lys
 465 470 475 480
 Pro Val Arg Ile Thr Asn Val Ala Pro Gly Val Lys Glu Gly Asp Val
 485 490 495
 Thr Asn Val Ala Gln Leu Lys Gly Val Ala Gln Asn Leu Asn Asn His
 500 505 510
 Ile Asp Asn Val Asp Gly Asn Ala Arg Ala Gly Ile Ala Gln Ala Ile
 515 520 525
 Ala Thr Ala Gly Leu Val Gln Ala Tyr Leu Pro Gly Lys Ser Met Met
 530 535 540
 Ala Ile Gly Gly Gly Thr Tyr Arg Gly Glu Ala Gly Tyr Ala Ile Gly
 545 550 555 560
 Tyr Ser Ser Ile Ser Asp Gly Gly Asn Trp Ile Ile Lys Gly Thr Ala
 565 570 575
 Ser Gly Asn Ser Arg Gly His Phe Gly Ala Ser Ala Ser Val Gly Tyr
 580 585 590

Gln Trp

<210> 94
 <211> 594
 <212> PRT
 <213> Neisseria meningitidis

<400> 94
 Met Asn Lys Ile Tyr Arg Ile Ile Trp Asn Ser Ala Leu Asn Ala Trp
 1 5 10 15
 Val Val Val Ser Glu Leu Thr Arg Asn His Thr Lys Arg Ala Ser Ala
 20 25 30
 Thr Val Ala Thr Ala Val Leu Ala Thr Leu Leu Phe Ala Thr Val Gln
 35 40 45
 Ala Asn Ala Thr Asp Asp Asp Asp Leu Tyr Leu Glu Pro Val Gln Arg
 50 55 60
 Thr Ala Val Val Leu Ser Phe Arg Ser Asp Lys Glu Gly Thr Gly Glu
 65 70 75 80
 Lys Glu Gly Thr Glu Asp Ser Asn Trp Ala Val Tyr Phe Asp Glu Lys
 85 90 95
 Arg Val Leu Lys Ala Gly Ala Ile Thr Leu Lys Ala Gly Asp Asn Leu
 100 105 110
 Lys Ile Lys Gln Asn Thr Asn Glu Asn Thr Asn Asp Ser Ser Phe Thr
 115 120 125

Tyr Ser Leu Lys Lys Asp Leu Thr Asp Leu Thr Ser Val Glu Thr Glu
130 135 140
Lys Leu Ser Phe Gly Ala Asn Gly Asn Lys Val Asn Ile Thr Ser Asp
145 150 155 160
Thr Lys Gly Leu Asn Phe Ala Lys Glu Thr Ala Gly Thr Asn Gly Asp
165 170 175
Pro Thr Val His Leu Asn Gly Ile Gly Ser Thr Leu Thr Asp Thr Leu
180 185 190
Leu Asn Thr Gly Ala Thr Thr Asn Val Thr Asn Asp Asn Val Thr Asp
195 200 205
Asp Glu Lys Lys Arg Ala Ala Ser Val Lys Asp Val Leu Asn Ala Gly
210 215 220
Trp Asn Ile Lys Gly Val Lys Pro Gly Thr Thr Ala Ser Asp Asn Val
225 230 235 240
Asp Phe Val Arg Thr Tyr Asp Thr Val Glu Phe Leu Ser Ala Asp Thr
245 250 255
Lys Thr Thr Thr Val Asn Val Glu Ser Lys Asp Asn Gly Lys Lys Thr
260 265 270
Glu Val Lys Ile Gly Ala Lys Thr Ser Val Ile Lys Glu Lys Asp Gly
275 280 285
Lys Leu Val Thr Gly Lys Gly Lys Asp Glu Asn Gly Ser Ser Thr Asp
290 295 300
Glu Gly Glu Gly Leu Val Thr Ala Lys Glu Val Ile Asp Ala Val Asn
305 310 315 320
Lys Ala Gly Trp Arg Met Lys Thr Thr Thr Ala Asn Gly Gln Thr Gly
325 330 335
Gln Ala Asp Lys Phe Glu Thr Val Thr Ser Gly Thr Asn Val Thr Phe
340 345 350
Ala Ser Gly Lys Gly Thr Thr Ala Thr Val Ser Lys Asp Asp Gln Gly
355 360 365
Asn Ile Thr Val Lys Tyr Asp Val Asn Val Gly Asp Ala Leu Asn Val
370 375 380
Asn Gln Leu Gln Asn Ser Gly Trp Asn Leu Asp Ser Lys Ala Val Ala
385 390 395 400
Gly Ser Ser Gly Lys Val Ile Ser Gly Asn Val Ser Pro Ser Lys Gly
405 410 415
Lys Met Asp Glu Thr Val Asn Ile Asn Ala Gly Asn Asn Ile Glu Ile
420 425 430

Thr Arg Asn Gly Lys Asn Ile Asp Ile Ala Thr Ser Met Ala Pro Gln
 435 440 445
 Phe Ser Ser Val Ser Leu Gly Ala Gly Ala Asp Ala Pro Thr Leu Ser
 450 455 460
 Val Asp Asp Glu Gly Ala Leu Asn Val Gly Ser Lys Asp Thr Asn Lys
 465 470 475 480
 Pro Val Arg Ile Thr Asn Val Ala Pro Gly Val Lys Glu Gly Asp Val
 485 490 495
 Thr Asn Val Ala Gln Leu Lys Gly Val Ala Gln Asn Leu Asn Asn Arg
 500 505 510
 Ile Asp Asn Val Asp Gly Asn Ala Arg Ala Gly Ile Ala Gln Ala Ile
 515 520 525
 Ala Thr Ala Gly Leu Val Gln Ala Tyr Leu Pro Gly Lys Ser Met Met
 530 535 540
 Ala Ile Gly Gly Asp Thr Tyr Arg Gly Glu Ala Gly Tyr Ala Ile Gly
 545 550 555 560
 Tyr Ser Ser Ile Ser Asp Gly Gly Asn Trp Ile Ile Lys Gly Thr Ala
 565 570 575
 Ser Gly Asn Ser Arg Gly His Phe Gly Ala Ser Ala Ser Val Gly Tyr
 580 585 590

Gln Trp

<210> 95
 <211> 591
 <212> PRT
 <213> Neisseria meningitidis
 <400> 95
 Met Asn Lys Ile Tyr Arg Ile Ile Trp Asn Ser Ala Leu Asn Ala Trp
 1 5 10 15
 Val Val Val Ser Glu Leu Thr Arg Asn His Thr Lys Arg Ala Ser Ala
 20 25 30
 Thr Val Glu Thr Ala Val Leu Ala Thr Leu Leu Phe Ala Thr Val Gln
 35 40 45
 Ala Ser Ala Asn Asn Glu Glu Gln Glu Glu Asp Leu Tyr Leu Asp Pro
 50 55 60
 Val Gln Arg Thr Val Ala Val Leu Ile Val Asn Ser Asp Lys Glu Gly
 65 70 75 80
 Thr Gly Glu Lys Glu Lys Val Glu Glu Asn Ser Asp Trp Ala Val Tyr
 85 90 95

Phe Asn Glu Lys Gly Val Leu Thr Ala Arg Glu Ile Thr Leu Lys Ala
100 105 110
Gly Asp Asn Leu Lys Ile Lys Gln Asn Gly Thr Asn Phe Thr Tyr Ser
115 120 125
Leu Lys Lys Asp Leu Thr Asp Leu Thr Ser Val Gly Thr Glu Lys Leu
130 135 140
Ser Phe Ser Ala Asn Gly Asn Lys Val Asn Ile Thr Ser Asp Thr Lys
145 150 155 160
Gly Leu Asn Phe Ala Lys Glu Thr Ala Gly Thr Asn Gly Asp Thr Thr
165 170 175
Val His Leu Asn Gly Ile Gly Ser Thr Leu Thr Asp Thr Leu Leu Asn
180 185 190
Thr Gly Ala Thr Thr Asn Val Thr Asn Asp Asn Val Thr Asp Asp Glu
195 200 205
Lys Lys Arg Ala Ala Ser Val Lys Asp Val Leu Asn Ala Gly Trp Asn
210 215 220
Ile Lys Gly Val Lys Pro Gly Thr Thr Ala Ser Asp Asn Val Asp Phe
225 230 235 240
Val Arg Thr Tyr Asp Thr Val Glu Phe Leu Ser Ala Asp Thr Lys Thr
245 250 255
Thr Thr Val Asn Val Glu Ser Lys Asp Asn Gly Lys Lys Thr Glu Val
260 265 270
Lys Ile Gly Ala Lys Thr Ser Val Ile Lys Glu Lys Asp Gly Lys Leu
275 280 285
Val Thr Gly Lys Asp Lys Gly Glu Asn Gly Ser Ser Thr Asp Glu Gly
290 295 300
Glu Gly Leu Val Thr Ala Lys Glu Val Ile Asp Ala Val Asn Lys Ala
305 310 315 320
Gly Trp Arg Met Lys Thr Thr Thr Ala Asn Gly Gln Thr Gly Gln Ala
325 330 335
Asp Lys Phe Glu Thr Val Thr Ser Gly Thr Asn Val Thr Phe Ala Ser
340 345 350
Gly Lys Gly Thr Thr Ala Thr Val Ser Lys Asp Asp Gln Gly Asn Ile
355 360 365
Thr Val Met Tyr Asp Val Asn Val Gly Asp Ala Leu Asn Val Asn Gln
370 375 380
Leu Gln Asn Ser Gly Trp Asn Leu Asp Ser Lys Ala Val Ala Gly Ser
385 390 395 400

Ser Gly Lys Val Ile Ser Gly Asn Val Ser Pro Ser Lys Gly Lys Met
 405 410 415
 Asp Glu Thr Val Asn Ile Asn Ala Gly Asn Asn Ile Glu Ile Thr Arg
 420 425 430
 Asn Gly Lys Asn Ile Asp Ile Ala Thr Ser Met Thr Pro Gln Phe Ser
 435 440 445
 Ser Val Ser Leu Gly Ala Gly Ala Asp Ala Pro Thr Leu Ser Val Asp
 450 455 460
 Gly Asp Ala Leu Asn Val Gly Ser Lys Lys Asp Asn Lys Pro Val Arg
 465 470 475 480
 Ile Thr Asn Val Ala Pro Gly Val Lys Glu Gly Asp Val Thr Asn Val
 485 490 495
 Ala Gln Leu Lys Gly Val Ala Gln Asn Leu Asn Asn Arg Ile Asp Asn
 500 505 510
 Val Asp Gly Asn Ala Arg Ala Gly Ile Ala Gln Ala Ile Ala Thr Ala
 515 520 525
 Gly Leu Val Gln Ala Tyr Leu Pro Gly Lys Ser Met Met Ala Ile Gly
 530 535 540
 Gly Gly Thr Tyr Arg Gly Glu Ala Gly Tyr Ala Ile Gly Tyr Ser Ser
 545 550 555 560
 Ile Ser Asp Gly Gly Asn Trp Ile Ile Lys Gly Thr Ala Ser Gly Asn
 565 570 575
 Ser Arg Gly His Phe Gly Ala Ser Ala Ser Val Gly Tyr Gln Trp
 580 585 590

<210> 96
 <211> 591
 <212> PRT
 <213> Neisseria meningitidis

<400> 96
 Met Asn Lys Ile Tyr Arg Ile Ile Trp Asn Ser Ala Leu Asn Ala Trp
 1 5 10 15
 Val Val Val Ser Glu Leu Thr Arg Asn His Thr Lys Arg Ala Ser Ala
 20 25 30
 Thr Val Lys Thr Ala Val Leu Ala Thr Leu Leu Phe Ala Thr Val Gln
 35 40 45
 Ala Ser Ala Asn Asn Glu Glu Gln Glu Glu Asp Leu Tyr Leu Asp Pro
 50 55 60
 Val Gln Arg Thr Val Ala Val Leu Ile Val Asn Ser Asp Lys Glu Gly

65	70	75	80
Thr Gly Glu Lys Glu Lys Val Glu Glu Asn Ser Asp Trp Ala Val Tyr	85	90	95
Phe Asn Glu Lys Gly Val Leu Thr Ala Arg Glu Ile Thr Leu Lys Ala	100	105	110
Gly Asp Asn Leu Lys Ile Lys Gln Asn Gly Thr Asn Phe Thr Tyr Ser	115	120	125
Leu Lys Lys Asp Leu Thr Asp Leu Thr Ser Val Gly Thr Glu Lys Leu	130	135	140
Ser Phe Ser Ala Asn Gly Asn Lys Val Asn Ile Thr Ser Asp Thr Lys	145	150	155
Gly Leu Asn Phe Ala Lys Glu Thr Ala Gly Thr Asn Gly Asp Thr Thr	165	170	175
Val His Leu Asn Gly Ile Gly Ser Thr Leu Thr Asp Thr Leu Leu Asn	180	185	190
Thr Gly Ala Thr Thr Asn Val Thr Asn Asp Asn Val Thr Asp Asp Glu	195	200	205
Lys Lys Arg Ala Ala Ser Val Lys Asp Val Leu Asn Ala Gly Trp Asn	210	215	220
Ile Lys Gly Val Lys Pro Gly Thr Thr Ala Ser Asp Asn Val Asp Phe	225	230	235
Val Arg Thr Tyr Asp Thr Val Glu Phe Leu Ser Ala Asp Thr Lys Thr	245	250	255
Thr Thr Val Asn Val Glu Ser Lys Asp Asn Gly Lys Lys Thr Glu Val	260	265	270
Lys Ile Gly Ala Lys Thr Ser Val Ile Lys Glu Lys Asp Gly Lys Leu	275	280	285
Val Thr Gly Lys Asp Lys Gly Glu Asn Gly Ser Ser Thr Asp Glu Gly	290	295	300
Glu Gly Leu Val Thr Ala Lys Glu Val Ile Asp Ala Val Asn Lys Ala	305	310	315
Gly Trp Arg Met Lys Thr Thr Thr Ala Asn Gly Gln Thr Gly Gln Ala	325	330	335
Asp Lys Phe Glu Thr Val Thr Ser Gly Thr Asn Val Thr Phe Ala Ser	340	345	350
Gly Lys Gly Thr Thr Ala Thr Val Ser Lys Asp Asp Gln Gly Asn Ile	355	360	365
Thr Val Met Tyr Asp Val Asn Val Gly Asp Ala Leu Asn Val Asn Gln			

370	375	380
Leu Gln Asn Ser Gly Trp Asn Leu Asp Ser Lys Ala Val Ala Gly Ser		
385	390	395 400
Ser Gly Lys Val Ile Ser Gly Asn Val Ser Pro Ser Lys Gly Lys Met		
	405	410 415
Asp Glu Thr Val Asn Ile Asn Ala Gly Asn Asn Ile Glu Ile Thr Arg		
	420	425 430
Asn Gly Lys Asn Ile Asp Ile Ala Thr Ser Met Thr Pro Gln Phe Ser		
	435	440 445
Ser Val Ser Leu Gly Ala Gly Ala Asp Ala Pro Thr Leu Ser Val Asp		
	450	455 460
Gly Asp Ala Leu Asn Val Gly Ser Lys Lys Asp Asn Lys Pro Val Arg		
465	470	475 480
Ile Thr Asn Val Ala Pro Gly Val Lys Glu Gly Asp Val Thr Asn Val		
	485	490 495
Ala Gln Leu Lys Gly Val Ala Gln Asn Leu Asn Asn Arg Ile Asp Asn		
	500	505 510
Val Asp Gly Asn Ala Arg Ala Gly Ile Ala Gln Ala Ile Ala Thr Ala		
	515	520 525
Gly Leu Val Gln Ala Tyr Leu Pro Gly Lys Ser Met Met Ala Ile Gly		
530	535	540
Gly Gly Thr Tyr Arg Gly Glu Ala Gly Tyr Ala Ile Gly Tyr Ser Ser		
545	550	555 560
Ile Ser Asp Gly Gly Asn Trp Ile Ile Lys Gly Thr Ala Ser Gly Asn		
	565	570 575
Ser Arg Gly His Phe Gly Ala Ser Ala Ser Val Gly Tyr Gln Trp		
	580	585 590

<210> 97
 <211> 595
 <212> PRT
 <213> Neisseria meningitidis

<400> 97
Met Asn Lys Ile Tyr Arg Ile Ile Trp Asn Ser Ala Leu Asn Ala Trp
1 5 10 15
Val Val Val Ser Glu Leu Thr Arg Asn His Thr Lys Arg Ala Ser Ala
20 25 30
Thr Val Glu Thr Ala Val Leu Ala Thr Leu Leu Phe Ala Thr Val Gln
35 40 45

Ala Asn Ala Thr Asp Thr Asp Glu Asp Asp Glu Leu Glu Pro Val Val
 50 55 60
 Arg Ser Ala Leu Val Leu Gln Phe Met Ile Asp Lys Glu Gly Asn Gly
 65 70 75 80
 Glu Ile Glu Ser Thr Gly Asp Ile Gly Trp Ser Ile Tyr Tyr Asp Asp
 85 90 95
 His Asn Thr Leu His Gly Ala Thr Val Thr Leu Lys Ala Gly Asp Asn
 100 105 110
 Leu Lys Ile Lys Gln Asn Thr Asp Glu Asn Thr Asn Ala Ser Ser Phe
 115 120 125
 Thr Tyr Ser Leu Lys Lys Asp Leu Thr Asp Leu Thr Ser Val Gly Thr
 130 135 140
 Glu Glu Leu Ser Phe Gly Ala Asn Gly Asn Lys Val Asn Ile Thr Ser
 145 150 155 160
 Asp Thr Lys Gly Leu Asn Phe Ala Lys Lys Thr Ala Gly Thr Asn Gly
 165 170 175
 Asp Thr Thr Val His Leu Asn Gly Ile Gly Ser Thr Leu Thr Asp Thr
 180 185 190
 Leu Ala Gly Ser Ser Ala Ser His Val Asp Ala Gly Asn Gln Ser Thr
 195 200 205
 His Tyr Thr Arg Ala Ala Ser Ile Lys Asp Val Leu Asn Ala Gly Trp
 210 215 220
 Asn Ile Lys Gly Val Lys Thr Gly Ser Thr Thr Gly Gln Ser Glu Asn
 225 230 235 240
 Val Asp Phe Val Arg Thr Tyr Asp Thr Val Glu Phe Leu Ser Ala Asp
 245 250 255
 Thr Lys Thr Thr Thr Val Asn Val Glu Ser Lys Asp Asn Gly Lys Arg
 260 265 270
 Thr Glu Val Lys Ile Gly Ala Lys Thr Ser Val Ile Lys Glu Lys Asp
 275 280 285
 Gly Lys Leu Val Thr Gly Lys Gly Lys Gly Glu Asn Gly Ser Ser Thr
 290 295 300
 Asp Glu Gly Glu Gly Leu Val Thr Ala Lys Glu Val Ile Asp Ala Val
 305 310 315 320
 Asn Lys Ala Gly Trp Arg Met Lys Thr Thr Thr Ala Asn Gly Gln Thr
 325 330 335
 Gly Gln Ala Asp Lys Phe Glu Thr Val Thr Ser Gly Thr Asn Val Thr
 340 345 350

Phe Ala Ser Gly Lys Gly Thr Thr Ala Thr Val Ser Lys Asp Asp Gln
355 360 365
Gly Asn Ile Thr Val Lys Tyr Asp Val Asn Val Gly Asp Ala Leu Asn
370 375 380
Val Asn Gln Leu Gln Asn Ser Gly Trp Asn Leu Asp Ser Lys Ala Val
385 390 395 400
Ala Gly Ser Ser Gly Lys Val Ile Ser Gly Asn Val Ser Pro Ser Lys
405 410 415
Gly Lys Met Asp Glu Thr Val Asn Ile Asn Ala Gly Asn Asn Ile Glu
420 425 430
Ile Thr Arg Asn Gly Lys Asn Ile Asp Ile Ala Thr Ser Met Thr Pro
435 440 445
Gln Phe Ser Ser Val Ser Leu Gly Ala Gly Ala Asp Ala Pro Thr Leu
450 455 460
Ser Val Asp Asp Glu Gly Ala Leu Asn Val Gly Ser Lys Asp Ala Asn
465 470 475 480
Lys Pro Val Arg Ile Thr Asn Val Ala Pro Gly Val Lys Glu Gly Asp
485 490 495
Val Thr Asn Val Ala Gln Leu Lys Gly Val Ala Gln Asn Leu Asn Asn
500 505 510
His Ile Asp Asn Val Asp Gly Asn Ala Arg Ala Gly Ile Ala Gln Ala
515 520 525
Ile Ala Thr Ala Gly Leu Val Gln Ala Tyr Leu Pro Gly Lys Ser Met
530 535 540
Met Ala Ile Gly Gly Gly Thr Tyr Arg Gly Glu Ala Gly Tyr Ala Ile
545 550 555 560
Gly Tyr Ser Ser Ile Ser Asp Gly Gly Asn Trp Ile Ile Lys Gly Thr
565 570 575
Ala Ser Gly Asn Ser Arg Gly His Phe Gly Ala Ser Ala Ser Val Gly
580 585 590
Tyr Gln Trp
595

<210> 98
<211> 592
<212> PRT
<213> Neisseria meningitidis

<400> 98
Met Asn Lys Ile Tyr Arg Ile Ile Trp Asn Ser Ala Leu Asn Ala Trp
1 5 10 15

Val	Ala	Val	Ser	Glu	Leu	Thr	Arg	Asn	His	Thr	Lys	Arg	Ala	Ser	Ala	20	25	30
Thr	Val	Lys	Thr	Ala	Val	Leu	Ala	Thr	Leu	Leu	Phe	Ala	Thr	Val	Gln	35	40	45
Ala	Asn	Ala	Thr	Asp	Glu	Asp	Glu	Glu	Glu	Glu	Leu	Glu	Ser	Val	Gln	50	55	60
Arg	Ser	Val	Val	Gly	Ser	Ile	Gln	Ala	Ser	Met	Glu	Gly	Ser	Gly	Glu	65	70	75
Leu	Glu	Thr	Ile	Ser	Leu	Ser	Met	Thr	Asn	Asp	Ser	Lys	Glu	Phe	Val	85	90	95
Asp	Pro	Tyr	Ile	Val	Val	Thr	Leu	Lys	Ala	Gly	Asp	Asn	Leu	Lys	Ile	100	105	110
Lys	Gln	Asn	Thr	Asn	Glu	Asn	Thr	Asn	Ala	Ser	Ser	Phe	Thr	Tyr	Ser	115	120	125
Leu	Lys	Lys	Asp	Leu	Thr	Gly	Leu	Ile	Asn	Val	Glu	Thr	Glu	Lys	Leu	130	135	140
Ser	Phe	Gly	Ala	Asn	Gly	Lys	Lys	Val	Asn	Ile	Ile	Ser	Asp	Thr	Lys	145	150	155
Gly	Leu	Asn	Phe	Ala	Lys	Glu	Thr	Ala	Gly	Thr	Asn	Gly	Asp	Thr	Thr	165	170	175
Val	His	Leu	Asn	Gly	Ile	Gly	Ser	Thr	Leu	Thr	Asp	Thr	Leu	Ala	Gly	180	185	190
Ser	Ser	Ala	Ser	His	Val	Asp	Ala	Gly	Asn	Gln	Ser	Thr	His	Tyr	Thr	195	200	205
Arg	Ala	Ala	Ser	Ile	Lys	Asp	Val	Leu	Asn	Ala	Gly	Trp	Asn	Ile	Lys	210	215	220
Gly	Val	Lys	Thr	Gly	Ser	Thr	Thr	Gly	Gln	Ser	Glu	Asn	Val	Asp	Phe	225	230	235
Val	Arg	Thr	Tyr	Asp	Thr	Val	Glu	Phe	Leu	Ser	Ala	Asp	Thr	Lys	Thr	245	250	255
Thr	Thr	Val	Asn	Val	Glu	Ser	Lys	Asp	Asn	Gly	Lys	Arg	Thr	Glu	Val	260	265	270
Lys	Ile	Gly	Ala	Lys	Thr	Ser	Val	Ile	Lys	Glu	Lys	Asp	Gly	Lys	Leu	275	280	285
Val	Thr	Gly	Lys	Gly	Lys	Gly	Glu	Asn	Gly	Ser	Ser	Thr	Asp	Glu	Gly	290	295	300
Glu	Gly	Leu	Val	Thr	Ala	Lys	Glu	Val	Ile	Asp	Ala	Val	Asn	Lys	Ala	305	310	315

Gly	Trp	Arg	Met	Lys	Thr	Thr	Thr	Ala	Asn	Gly	Gln	Thr	Gly	Gln	Ala	
				325					330					335		
Asp	Lys	Phe	Glu	Thr	Val	Thr	Ser	Gly	Thr	Asn	Val	Thr	Phe	Ala	Ser	
			340					345					350			
Gly	Lys	Gly	Thr	Thr	Ala	Thr	Val	Ser	Lys	Asp	Asp	Gln	Gly	Asn	Ile	
		355					360					365				
Thr	Val	Met	Tyr	Asp	Val	Asn	Val	Gly	Asp	Ala	Leu	Asn	Val	Asn	Gln	
	370					375					380					
Leu	Gln	Asn	Ser	Gly	Trp	Asn	Leu	Asp	Ser	Lys	Ala	Val	Ala	Gly	Ser	
385					390					395					400	
Ser	Gly	Lys	Val	Ile	Ser	Gly	Asn	Val	Ser	Pro	Ser	Lys	Gly	Lys	Met	
			405						410					415		
Asp	Glu	Thr	Val	Asn	Ile	Asn	Ala	Gly	Asn	Asn	Ile	Glu	Ile	Ser	Arg	
			420					425					430			
Asn	Gly	Lys	Asn	Ile	Asp	Ile	Ala	Thr	Ser	Met	Ala	Pro	Gln	Phe	Ser	
		435					440					445				
Ser	Val	Ser	Leu	Gly	Ala	Gly	Ala	Asp	Ala	Pro	Thr	Leu	Ser	Val	Asp	
	450					455					460					
Asp	Glu	Gly	Ala	Leu	Asn	Val	Gly	Ser	Lys	Asp	Ala	Asn	Lys	Pro	Val	
465				470						475					480	
Arg	Ile	Thr	Asn	Val	Ala	Pro	Gly	Val	Lys	Glu	Gly	Asp	Val	Thr	Asn	
			485						490					495		
Val	Ala	Gln	Leu	Lys	Gly	Val	Ala	Gln	Asn	Leu	Asn	Asn	Arg	Ile	Asp	
		500						505					510			
Asn	Val	Asp	Gly	Asn	Ala	Arg	Ala	Gly	Ile	Ala	Gln	Ala	Ile	Ala	Thr	
		515					520					525				
Ala	Gly	Leu	Val	Gln	Ala	Tyr	Leu	Pro	Gly	Lys	Ser	Met	Met	Ala	Ile	
	530					535					540					
Gly	Gly	Gly	Thr	Tyr	Arg	Gly	Glu	Ala	Gly	Tyr	Ala	Ile	Gly	Tyr	Ser	
545				550						555					560	
Ser	Ile	Ser	Asp	Gly	Gly	Asn	Trp	Ile	Ile	Lys	Gly	Thr	Ala	Ser	Gly	
			565						570					575		
Asn	Ser	Arg	Gly	His	Phe	Gly	Ala	Ser	Ala	Ser	Val	Gly	Tyr	Gln	Trp	
			580					585					590			

<210> 99
<211> 594

<212> PRT
 <213> Neisseria meningitidis

<400> 99

Met	Asn	Lys	Ile	Tyr	Arg	Ile	Ile	Trp	Asn	Ser	Ala	Leu	Asn	Ala	Trp	1	5	10	15
Val	Val	Val	Ser	Glu	Leu	Thr	Arg	Asn	His	Thr	Lys	Arg	Ala	Ser	Ala	20	25	30	
Thr	Val	Ala	Thr	Ala	Val	Leu	Ala	Thr	Leu	Leu	Phe	Ala	Thr	Val	Gln	35	40	45	
Ala	Ser	Thr	Thr	Asp	Asp	Asp	Asp	Leu	Tyr	Leu	Glu	Pro	Val	Gln	Arg	50	55	60	
Thr	Ala	Pro	Val	Leu	Ser	Phe	His	Ala	Asp	Ser	Glu	Gly	Thr	Gly	Glu	65	70	75	80
Lys	Glu	Val	Thr	Glu	Asp	Ser	Asn	Trp	Gly	Val	Tyr	Phe	Asp	Lys	Lys	85	90	95	
Gly	Val	Leu	Thr	Ala	Gly	Thr	Ile	Thr	Leu	Lys	Ala	Gly	Asp	Asn	Leu	100	105	110	
Lys	Ile	Lys	Gln	Asn	Thr	Asp	Glu	Asn	Thr	Asn	Ala	Ser	Ser	Phe	Thr	115	120	125	
Tyr	Ser	Leu	Lys	Lys	Asp	Leu	Thr	Asp	Leu	Thr	Ser	Val	Glu	Thr	Glu	130	135	140	
Lys	Leu	Ser	Phe	Gly	Ala	Asn	Gly	Lys	Lys	Val	Asn	Ile	Thr	Ser	Asp	145	150	155	160
Thr	Lys	Gly	Leu	Asn	Phe	Ala	Lys	Glu	Thr	Ala	Gly	Thr	Asn	Gly	Asp	165	170	175	
Thr	Thr	Val	His	Leu	Asn	Gly	Ile	Gly	Ser	Thr	Leu	Thr	Asp	Thr	Leu	180	185	190	
Leu	Asn	Thr	Gly	Ala	Thr	Thr	Asn	Val	Thr	Asn	Asp	Asn	Val	Thr	Asp	195	200	205	
Asp	Glu	Lys	Lys	Arg	Ala	Ala	Ser	Val	Lys	Asp	Val	Leu	Asn	Ala	Gly	210	215	220	
Trp	Asn	Ile	Lys	Gly	Val	Lys	Pro	Gly	Thr	Thr	Ala	Ser	Asp	Asn	Val	225	230	235	240
Asp	Phe	Val	Arg	Thr	Tyr	Asp	Thr	Val	Glu	Phe	Leu	Ser	Ala	Asp	Thr	245	250	255	
Lys	Thr	Thr	Thr	Val	Asn	Val	Glu	Ser	Lys	Asp	Asn	Gly	Lys	Lys	Thr	260	265	270	
Glu	Val	Lys	Ile	Gly	Ala	Lys	Thr	Ser	Val	Ile	Lys	Glu	Lys	Asp	Gly	275	280	285	

Lys Leu Val Thr Gly Lys Asp Lys Gly Glu Asn Gly Ser Ser Thr Asp
 290 295 300
 Glu Gly Glu Gly Leu Val Thr Ala Lys Glu Val Ile Asp Ala Val Asn
 305 310 315 320
 Lys Ala Gly Trp Arg Met Lys Thr Thr Thr Ala Asn Gly Gln Thr Gly
 325 330 335
 Gln Ala Asp Lys Phe Glu Thr Val Thr Ser Gly Thr Lys Val Thr Phe
 340 345 350
 Ala Ser Gly Asn Gly Thr Thr Ala Thr Val Ser Lys Asp Asp Gln Gly
 355 360 365
 Asn Ile Thr Val Lys Tyr Asp Val Asn Val Gly Asp Ala Leu Asn Val
 370 375 380
 Asn Gln Leu Gln Asn Ser Gly Trp Asn Leu Asp Ser Lys Ala Val Ala
 385 390 395 400
 Gly Ser Ser Gly Lys Val Ile Ser Gly Asn Val Ser Pro Ser Lys Gly
 405 410 415
 Lys Met Asp Glu Thr Val Asn Ile Asn Ala Gly Asn Asn Ile Glu Ile
 420 425 430
 Thr Arg Asn Gly Lys Asn Ile Asp Ile Ala Thr Ser Met Thr Pro Gln
 435 440 445
 Phe Ser Ser Val Ser Leu Gly Ala Gly Ala Asp Ala Pro Thr Leu Ser
 450 455 460
 Val Asp Asp Glu Gly Ala Leu Asn Val Gly Ser Lys Asp Ala Asn Lys
 465 470 475 480
 Pro Val Arg Ile Thr Asn Val Ala Pro Gly Val Lys Glu Gly Asp Val
 485 490 495
 Thr Asn Val Ala Gln Leu Lys Gly Val Ala Gln Asn Leu Asn Asn His
 500 505 510
 Ile Asp Asn Val Asp Gly Asn Ala Arg Ala Gly Ile Ala Gln Ala Ile
 515 520 525
 Ala Thr Ala Ser Leu Val Gln Ala Tyr Leu Pro Gly Lys Ser Met Met
 530 535 540
 Ala Ile Gly Gly Gly Thr Tyr Arg Gly Glu Ala Gly Tyr Ala Ile Gly
 545 550 555 560
 Tyr Ser Ser Ile Ser Asp Gly Gly Asn Trp Ile Ile Lys Gly Thr Ala
 565 570 575
 Ser Gly Asn Ser Arg Gly His Phe Gly Ala Ser Ala Ser Val Gly Tyr
 580 585 590

Gln Trp

<210> 100

<211> 599

<212> PRT

<213> Neisseria meningitidis

<400> 100

Met Asn Lys Ile Tyr Arg Ile Ile Trp Asn Ser Ala Leu Asn Ala Trp
1 5 10 15

Val Ala Val Ser Glu Leu Thr Arg Asn His Thr Lys Arg Ala Ser Ala
20 25 30

Thr Val Lys Thr Ala Val Leu Ala Thr Leu Leu Phe Ala Thr Val Gln
35 40 45

Ala Asn Ala Thr Asp Glu Asp Glu Glu Glu Glu Leu Glu Pro Val Val
50 55 60

Arg Ser Ala Leu Val Leu Gln Phe Met Ile Asp Lys Glu Gly Asn Gly
65 70 75 80

Glu Asn Glu Ser Thr Gly Asn Ile Gly Trp Ser Ile Tyr Tyr Asp Asn
85 90 95

His Asn Thr Leu His Gly Ala Thr Val Thr Leu Lys Ala Gly Asp Asn
100 105 110

Leu Lys Ile Lys Gln Asn Thr Asn Lys Asn Thr Asn Glu Asn Thr Asn
115 120 125

Asp Ser Ser Phe Thr Tyr Ser Leu Lys Lys Asp Leu Thr Asp Leu Thr
130 135 140

Ser Val Glu Thr Glu Lys Leu Ser Phe Gly Ala Asn Gly Asn Lys Val
145 150 155 160

Asn Ile Thr Ser Asp Thr Lys Gly Leu Asn Phe Ala Lys Glu Thr Ala
165 170 175

Gly Thr Asn Gly Asp Thr Thr Val His Leu Asn Gly Ile Gly Ser Thr
180 185 190

Leu Thr Asp Thr Leu Leu Asn Thr Gly Ala Thr Thr Asn Val Thr Asn
195 200 205

Asp Asn Val Thr Asp Asp Lys Lys Lys Arg Ala Ala Ser Val Lys Asp
210 215 220

Val Leu Asn Ala Gly Trp Asn Ile Lys Gly Val Lys Pro Gly Thr Thr
225 230 235 240

Ala Ser Asp Asn Val Asp Phe Val His Thr Tyr Asp Thr Val Glu Phe
245 250 255

Leu Ser Ala Asp Thr Lys Thr Thr Thr Val Asn Val Glu Ser Lys Asp
 260 265 270
 Asn Gly Lys Arg Thr Glu Val Lys Ile Gly Ala Lys Thr Ser Val Ile
 275 280 285
 Lys Glu Lys Asp Gly Lys Leu Val Thr Gly Lys Gly Lys Gly Glu Asn
 290 295 300
 Gly Ser Ser Thr Asp Glu Gly Glu Gly Leu Val Thr Ala Lys Glu Val
 305 310 315 320
 Ile Asp Ala Val Asn Lys Ala Gly Trp Arg Met Lys Thr Thr Thr Ala
 325 330 335
 Asn Gly Gln Thr Gly Gln Ala Asp Lys Phe Glu Thr Val Thr Ser Gly
 340 345 350
 Thr Asn Val Thr Phe Ala Ser Gly Lys Gly Thr Thr Ala Thr Val Ser
 355 360 365
 Lys Asp Asp Gln Gly Asn Ile Thr Val Lys Tyr Asp Val Asn Val Gly
 370 375 380
 Asp Ala Leu Asn Val Asn Gln Leu Gln Asn Ser Gly Trp Asn Leu Asp
 385 390 395 400
 Ser Lys Ala Val Ala Gly Ser Ser Gly Lys Val Ile Ser Gly Asn Val
 405 410 415
 Ser Pro Ser Lys Gly Lys Met Asp Glu Thr Val Asn Ile Asn Ala Gly
 420 425 430
 Asn Asn Ile Glu Ile Thr Arg Asn Gly Lys Asn Ile Asp Ile Ala Thr
 435 440 445
 Ser Met Thr Pro Gln Phe Ser Ser Val Ser Leu Gly Ala Gly Ala Asp
 450 455 460
 Ala Pro Thr Leu Ser Val Asp Asp Lys Gly Ala Leu Asn Val Gly Ser
 465 470 475 480
 Lys Asp Ala Asn Lys Pro Val Arg Ile Thr Asn Val Ala Pro Gly Val
 485 490 495
 Lys Glu Gly Asp Val Thr Asn Val Ala Gln Leu Lys Gly Val Ala Gln
 500 505 510
 Asn Leu Asn Asn Arg Ile Asp Asn Val Asp Gly Asn Ala Arg Ala Gly
 515 520 525
 Ile Ala Gln Ala Ile Ala Thr Ala Gly Leu Val Gln Ala Tyr Leu Pro
 530 535 540
 Gly Lys Ser Met Met Ala Ile Gly Gly Gly Thr Tyr Arg Gly Glu Ala
 545 550 555 560

Gly Tyr Ala Ile Gly Tyr Ser Ser Ile Ser Asp Gly Gly Asn Trp Ile
565 570 575

Ile Lys Gly Thr Ala Ser Gly Asn Ser Arg Gly His Phe Gly Ala Ser
580 585 590

Ala Ser Val Gly Tyr Gln Trp
595

<210> 101
<211> 598
<212> PRT
<213> Neisseria meningitidis

<400> 101
Met Asn Lys Ile Tyr Arg Ile Ile Trp Asn Ser Ala Leu Asn Ala Trp
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Val Val Val Ser Glu Leu Thr Arg Asn His Thr Lys Arg Ala Ser Ala
20 25 30

Thr Val Ala Thr Ala Val Leu Ala Thr Leu Leu Phe Ala Thr Val Gln
35 40 45

Ala Asn Ala Thr Asp Asp Asp Asp Leu Tyr Leu Glu Pro Val Gln Arg
50 55 60

Thr Ala Val Val Leu Ser Phe Arg Ser Asp Lys Glu Gly Thr Gly Glu
65 70 75 80

Lys Glu Gly Thr Glu Asp Ser Asn Trp Ala Val Tyr Phe Asp Glu Lys
85 90 95

Arg Val Leu Lys Ala Gly Ala Ile Thr Leu Lys Ala Gly Asp Asn Leu
100 105 110

Lys Ile Lys Gln Asn Thr Asn Glu Asn Thr Asn Glu Asn Thr Asn Asp
115 120 125

Ser Ser Phe Thr Tyr Ser Leu Lys Lys Asp Leu Thr Asp Leu Thr Ser
130 135 140

Val Glu Thr Glu Lys Leu Ser Phe Gly Ala Asn Gly Asn Lys Val Asn
145 150 155 160

Ile Thr Ser Asp Thr Lys Gly Leu Asn Phe Ala Lys Glu Thr Ala Gly
165 170 175

Thr Asn Gly Asp Pro Thr Val His Leu Asn Gly Ile Gly Ser Thr Leu
180 185 190

Thr Asp Thr Leu Leu Asn Thr Gly Ala Thr Thr Asn Val Thr Asn Asp
195 200 205

Asn Val Thr Asp Asp Glu Lys Lys Arg Ala Ala Ser Val Lys Asp Val
210 215 220

Leu	Asn	Ala	Gly	Trp	Asn	Ile	Lys	Gly	Val	Lys	Pro	Gly	Thr	Thr	Ala	225	230	235	240
Ser	Asp	Asn	Val	Asp	Phe	Val	Arg	Thr	Tyr	Asp	Thr	Val	Glu	Phe	Leu	245	250	255	
Ser	Ala	Asp	Thr	Lys	Thr	Thr	Thr	Val	Asn	Val	Glu	Ser	Lys	Asp	Asn	260	265	270	
Gly	Lys	Lys	Thr	Glu	Val	Lys	Ile	Gly	Ala	Lys	Thr	Ser	Val	Ile	Lys	275	280	285	
Glu	Lys	Asp	Gly	Lys	Leu	Val	Thr	Gly	Lys	Gly	Lys	Asp	Glu	Asn	Gly	290	295	300	
Ser	Ser	Thr	Asp	Glu	Gly	Glu	Gly	Leu	Val	Thr	Ala	Lys	Glu	Val	Ile	305	310	315	320
Asp	Ala	Val	Asn	Lys	Ala	Gly	Trp	Arg	Met	Lys	Thr	Thr	Thr	Ala	Asn	325	330	335	
Gly	Gln	Thr	Gly	Gln	Ala	Asp	Lys	Phe	Glu	Thr	Val	Thr	Ser	Gly	Thr	340	345	350	
Lys	Val	Thr	Phe	Ala	Ser	Gly	Asn	Gly	Thr	Thr	Ala	Thr	Val	Ser	Lys	355	360	365	
Asp	Asp	Gln	Gly	Asn	Ile	Thr	Val	Lys	Tyr	Asp	Val	Asn	Val	Gly	Asp	370	375	380	
Ala	Leu	Asn	Val	Asn	Gln	Leu	Gln	Asn	Ser	Gly	Trp	Asn	Leu	Asp	Ser	385	390	395	400
Lys	Ala	Val	Ala	Gly	Ser	Ser	Gly	Lys	Val	Ile	Ser	Gly	Asn	Val	Ser	405	410	415	
Pro	Ser	Lys	Gly	Lys	Met	Asp	Glu	Thr	Val	Asn	Ile	Asn	Ala	Gly	Asn	420	425	430	
Asn	Ile	Glu	Ile	Thr	Arg	Asn	Gly	Lys	Asn	Ile	Asp	Ile	Ala	Thr	Ser	435	440	445	
Met	Thr	Pro	Gln	Phe	Ser	Ser	Val	Ser	Leu	Gly	Ala	Gly	Ala	Asp	Ala	450	455	460	
Pro	Thr	Leu	Ser	Val	Asp	Asp	Glu	Gly	Ala	Leu	Asn	Val	Gly	Ser	Lys	465	470	475	480
Asp	Ala	Asn	Lys	Pro	Val	Arg	Ile	Thr	Asn	Val	Ala	Pro	Gly	Val	Lys	485	490	495	
Glu	Gly	Asp	Val	Thr	Asn	Val	Ala	Gln	Leu	Lys	Gly	Val	Ala	Gln	Asn	500	505	510	
Leu	Asn	Asn	Arg	Ile	Asp	Asn	Val	Asp	Gly	Asn	Ala	Arg	Ala	Gly	Ile	515	520	525	

Ala Gln Ala Ile Ala Thr Ala Gly Leu Ala Gln Ala Tyr Leu Pro Gly
 530 535 540

Lys Ser Met Met Ala Ile Gly Gly Gly Thr Tyr Arg Gly Glu Ala Gly
 545 550 555 560

Tyr Ala Ile Gly Tyr Ser Ser Ile Ser Asp Thr Gly Asn Trp Val Ile
 565 570 575

Lys Gly Thr Ala Ser Gly Asn Ser Arg Gly His Phe Gly Ala Ser Ala
 580 585 590

Ser Val Gly Tyr Gln Trp
 595

<210> 102
 <211> 594
 <212> PRT
 <213> Neisseria meningitidis

<400> 102
 Met Asn Lys Ile Tyr Arg Ile Ile Trp Asn Ser Ala Leu Asn Ala Trp
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Val Ala Val Ser Glu Leu Thr Arg Asn His Thr Lys Arg Ala Ser Ala
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Thr Val Ala Thr Ala Val Leu Ala Thr Leu Leu Phe Ala Thr Val Gln
 35 40 45

Ala Ser Thr Thr Asp Asp Asp Asp Leu Tyr Leu Glu Pro Val Gln Arg
 50 55 60

Thr Ala Pro Val Leu Ser Phe His Ala Asp Ser Glu Gly Thr Gly Glu
 65 70 75 80

Lys Glu Val Thr Glu Asp Ser Asn Trp Gly Val Tyr Phe Asp Lys Lys
 85 90 95

Gly Val Leu Thr Ala Gly Thr Ile Thr Leu Lys Ala Gly Asp Asn Leu
 100 105 110

Lys Ile Lys Gln Asn Thr Asp Glu Asn Thr Asn Ala Ser Ser Phe Thr
 115 120 125

Tyr Ser Leu Lys Lys Asp Leu Thr Asp Leu Thr Ser Val Glu Thr Glu
 130 135 140

Lys Leu Ser Phe Gly Ala Asn Gly Lys Lys Val Asn Ile Thr Ser Asp
 145 150 155 160

Thr Lys Gly Leu Asn Phe Ala Lys Glu Thr Ala Gly Thr Asn Gly Asp
 165 170 175

Thr Thr Val His Leu Asn Gly Ile Gly Ser Thr Leu Thr Asp Thr Leu

180					185					190					
Leu	Asn	Thr	Gly	Ala	Thr	Thr	Asn	Val	Thr	Asn	Asp	Asn	Val	Thr	Asp
	195						200					205			
Asp	Glu	Lys	Lys	Arg	Ala	Ala	Ser	Val	Lys	Asp	Val	Leu	Asn	Ala	Gly
	210					215					220				
Trp	Asn	Ile	Lys	Gly	Val	Lys	Pro	Gly	Thr	Thr	Ala	Ser	Asp	Asn	Val
	225					230					235				240
Asp	Phe	Val	Arg	Thr	Tyr	Asp	Thr	Val	Glu	Phe	Leu	Ser	Ala	Asp	Thr
				245					250					255	
Lys	Thr	Thr	Thr	Val	Asn	Val	Glu	Ser	Lys	Asp	Asn	Gly	Lys	Lys	Thr
			260					265					270		
Glu	Val	Lys	Ile	Gly	Ala	Lys	Thr	Ser	Val	Ile	Lys	Glu	Lys	Asp	Gly
		275					280					285			
Lys	Leu	Val	Thr	Gly	Lys	Asp	Lys	Gly	Glu	Asn	Gly	Ser	Ser	Thr	Asp
	290					295					300				
Glu	Gly	Glu	Gly	Leu	Val	Thr	Ala	Lys	Glu	Val	Ile	Asp	Ala	Val	Asn
	305					310					315				320
Lys	Ala	Gly	Trp	Arg	Met	Lys	Thr	Thr	Thr	Ala	Asn	Gly	Gln	Thr	Gly
				325					330					335	
Gln	Ala	Asp	Lys	Phe	Glu	Thr	Val	Thr	Ser	Gly	Thr	Lys	Val	Thr	Phe
			340					345					350		
Ala	Ser	Gly	Asn	Gly	Thr	Thr	Ala	Thr	Val	Ser	Lys	Asp	Asp	Gln	Gly
		355					360					365			
Asn	Ile	Thr	Val	Lys	Tyr	Asp	Val	Asn	Val	Gly	Asp	Ala	Leu	Asn	Val
	370					375					380				
Asn	Gln	Leu	Gln	Asn	Ser	Gly	Trp	Asn	Leu	Asp	Ser	Lys	Ala	Val	Ala
	385					390					395				400
Gly	Ser	Ser	Gly	Lys	Val	Ile	Ser	Gly	Asn	Val	Ser	Pro	Ser	Lys	Gly
				405					410					415	
Lys	Met	Asp	Glu	Thr	Val	Asn	Ile	Asn	Ala	Gly	Asn	Asn	Ile	Glu	Ile
			420					425					430		
Thr	Arg	Asn	Gly	Lys	Asn	Ile	Asp	Ile	Ala	Thr	Ser	Met	Thr	Pro	Gln
			435				440					445			
Phe	Ser	Ser	Val	Ser	Leu	Gly	Ala	Gly	Ala	Asp	Ala	Pro	Thr	Leu	Ser
	450					455					460				
Val	Asp	Asp	Glu	Gly	Ala	Leu	Asn	Val	Gly	Ser	Lys	Asp	Ala	Asn	Lys
	465					470					475				480
Pro	Val	Arg	Ile	Thr	Asn	Val	Ala	Pro	Gly	Val	Lys	Glu	Gly	Asp	Val

485										490					495															
Thr	Asn	Val	Ala	Gln	Leu	Lys	Gly	Val	Ala	Gln	Asn	Leu	Asn	Asn	His															
			500					505					510																	
Ile	Asp	Asn	Val	Asp	Gly	Asn	Ala	Arg	Ala	Gly	Ile	Ala	Gln	Ala	Ile															
		515					520					525																		
Ala	Thr	Ala	Gly	Leu	Val	Gln	Ala	Tyr	Leu	Pro	Gly	Lys	Ser	Met	Met															
		530				535					540																			
Ala	Ile	Gly	Gly	Gly	Thr	Tyr	Arg	Gly	Glu	Ala	Gly	Tyr	Ala	Ile	Gly															
545					550					555					560															
Tyr	Ser	Ser	Ile	Ser	Asp	Gly	Gly	Asn	Trp	Ile	Ile	Lys	Gly	Thr	Ala															
			565					570						575																
Ser	Gly	Asn	Ser	Arg	Gly	His	Phe	Gly	Ala	Ser	Ala	Ser	Val	Gly	Tyr															
		580						585					590																	

Gln Trp

<210> 103
 <211> 591
 <212> PRT
 <213> Neisseria meningitidis

<400> 103

Met	Asn	Lys	Ile	Tyr	Arg	Ile	Ile	Trp	Asn	Ser	Ala	Leu	Asn	Ala	Trp														
1				5				10					15																
Val	Val	Val	Ser	Glu	Leu	Thr	Arg	Asn	His	Thr	Lys	Arg	Ala	Ser	Ala														
			20					25					30																
Thr	Val	Lys	Thr	Ala	Val	Leu	Ala	Thr	Leu	Leu	Phe	Ala	Thr	Val	Gln														
		35					40					45																	
Ala	Ser	Ala	Asn	Asn	Glu	Glu	Gln	Glu	Glu	Asp	Leu	Tyr	Leu	Asp	Pro														
		50				55				60																			
Val	Gln	Arg	Thr	Val	Ala	Val	Leu	Ile	Val	Asn	Ser	Asp	Lys	Glu	Gly														
65					70				75					80															
Thr	Gly	Glu	Lys	Glu	Lys	Val	Glu	Glu	Asn	Ser	Asp	Trp	Ala	Val	Tyr														
			85					90					95																
Phe	Asn	Glu	Lys	Gly	Val	Leu	Thr	Ala	Arg	Glu	Ile	Thr	Leu	Lys	Ala														
		100					105					110																	
Gly	Asp	Asn	Leu	Lys	Ile	Lys	Gln	Asn	Gly	Thr	Asn	Phe	Thr	Tyr	Ser														
		115					120					125																	
Leu	Lys	Lys	Asp	Leu	Thr	Asp	Leu	Thr	Ser	Val	Gly	Thr	Glu	Lys	Leu														
		130				135					140																		

Ser	Phe	Ser	Ala	Asn	Gly	Asn	Lys	Val	Asn	Ile	Thr	Ser	Asp	Thr	Lys
145					150					155					160
Gly	Leu	Asn	Phe	Ala	Lys	Glu	Thr	Ala	Gly	Thr	Asn	Gly	Asp	Thr	Thr
				165					170					175	
Val	His	Leu	Asn	Gly	Ile	Gly	Ser	Thr	Leu	Thr	Asp	Thr	Leu	Leu	Asn
			180					185					190		
Thr	Gly	Ala	Thr	Thr	Asn	Val	Thr	Asn	Asp	Asn	Val	Thr	Asp	Asp	Glu
		195					200					205			
Lys	Lys	Arg	Ala	Ala	Ser	Val	Lys	Asp	Val	Leu	Asn	Ala	Gly	Trp	Asn
	210					215					220				
Ile	Lys	Gly	Val	Lys	Pro	Gly	Thr	Thr	Ala	Ser	Asp	Asn	Val	Asp	Phe
225					230					235					240
Val	Arg	Thr	Tyr	Asp	Thr	Val	Glu	Phe	Leu	Ser	Ala	Asp	Thr	Lys	Thr
				245					250					255	
Thr	Thr	Val	Asn	Val	Glu	Ser	Lys	Asp	Asn	Gly	Lys	Lys	Thr	Glu	Val
			260					265					270		
Lys	Ile	Gly	Ala	Lys	Thr	Ser	Val	Ile	Lys	Glu	Lys	Asp	Gly	Lys	Leu
		275					280					285			
Val	Thr	Gly	Lys	Asp	Lys	Gly	Glu	Asn	Gly	Ser	Ser	Thr	Asp	Glu	Gly
	290					295					300				
Glu	Gly	Leu	Val	Thr	Ala	Lys	Glu	Val	Ile	Asp	Ala	Val	Asn	Lys	Ala
305					310					315					320
Gly	Trp	Arg	Met	Lys	Thr	Thr	Thr	Ala	Asn	Gly	Gln	Thr	Gly	Gln	Ala
				325					330					335	
Asp	Lys	Phe	Glu	Thr	Val	Thr	Ser	Gly	Thr	Asn	Val	Thr	Phe	Ala	Ser
			340					345					350		
Gly	Lys	Gly	Thr	Thr	Ala	Thr	Val	Ser	Lys	Asp	Asp	Gln	Gly	Asn	Ile
		355					360					365			
Thr	Val	Met	Tyr	Asp	Val	Asn	Val	Gly	Asp	Ala	Leu	Asn	Val	Asn	His
	370					375					380				
Leu	Gln	Asn	Ser	Gly	Trp	Asp	Leu	Asp	Ser	Lys	Ala	Val	Ala	Gly	Ser
385					390					395					400
Ser	Gly	Lys	Val	Ile	Ser	Gly	Asn	Val	Ser	Pro	Ser	Lys	Gly	Lys	Met
			405						410					415	
Asp	Glu	Thr	Val	Asn	Ile	Asn	Ala	Gly	Asn	Asn	Ile	Glu	Ile	Thr	Arg
			420					425					430		
Asn	Gly	Lys	Asn	Ile	Asp	Ile	Ala	Thr	Ser	Met	Thr	Pro	Gln	Phe	Ser
		435					440					445			

Ser Val Ser Leu Gly Ala Gly Ala Asp Ala Pro Thr Leu Ser Val Asp
 450 455 460
 Gly Asp Ala Leu Asn Val Gly Ser Lys Lys Asp Asn Lys Pro Val Arg
 465 470 475 480
 Ile Thr Asn Val Ala Pro Gly Val Lys Glu Gly Asp Val Thr Asn Val
 485 490 495
 Ala Gln Leu Lys Gly Val Ala Gln Asn Leu Asn Asn Arg Ile Asp Asn
 500 505 510
 Val Asp Gly Asn Ala Arg Ala Gly Ile Ala Gln Ala Ile Ala Thr Ala
 515 520 525
 Gly Leu Val Gln Ala Tyr Leu Pro Gly Lys Ser Met Met Ala Ile Gly
 530 535 540
 Gly Gly Thr Tyr Arg Gly Glu Ala Gly Tyr Ala Ile Gly Tyr Ser Ser
 545 550 555 560
 Ile Ser Asp Gly Gly Asn Trp Ile Ile Lys Gly Thr Ala Ser Gly Asn
 565 570 575
 Ser Arg Gly His Phe Gly Ala Ser Ala Ser Val Gly Tyr Gln Trp
 580 585 590

<210> 104
 <211> 591
 <212> PRT
 <213> Neisseria meningitidis

<400> 104
 Met Asn Lys Ile Tyr Arg Ile Ile Trp Asn Ser Ala Leu Asn Ala Trp
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 Val Val Val Ser Glu Leu Thr Arg Asn His Thr Lys Arg Ala Ser Ala
 20 25 30
 Thr Val Lys Thr Ala Val Leu Ala Thr Leu Leu Phe Ala Thr Val Gln
 35 40 45
 Ala Ser Ala Asn Asn Glu Glu Gln Glu Glu Asp Leu Tyr Leu Asp Pro
 50 55 60
 Val Gln Arg Thr Val Ala Val Leu Ile Val Asn Ser Asp Lys Glu Gly
 65 70 75 80
 Thr Gly Glu Lys Glu Lys Val Glu Glu Asn Ser Asp Trp Ala Val Tyr
 85 90 95
 Phe Asn Glu Lys Gly Val Leu Thr Ala Arg Glu Ile Thr Leu Lys Ala
 100 105 110
 Gly Asp Asn Leu Lys Ile Lys Gln Asn Gly Thr Asn Phe Thr Tyr Ser
 115 120 125

Leu Lys Lys Asp Leu Thr Asp Leu Thr Ser Val Gly Thr Glu Lys Leu
 130 135 140
 Ser Phe Ser Ala Asn Gly Asn Lys Val Asn Ile Thr Ser Asp Thr Lys
 145 150 155 160
 Gly Leu Asn Phe Ala Lys Glu Thr Ala Gly Thr Asn Gly Asp Thr Thr
 165 170 175
 Val His Leu Asn Gly Ile Gly Ser Thr Leu Thr Asp Thr Leu Leu Asn
 180 185 190
 Thr Gly Ala Thr Thr Asn Val Thr Asn Asp Asn Val Thr Asp Asp Glu
 195 200 205
 Lys Lys Arg Ala Ala Ser Val Lys Asp Val Leu Asn Ala Gly Trp Asn
 210 215 220
 Ile Lys Gly Val Lys Pro Gly Thr Thr Ala Ser Asp Asn Val Asp Phe
 225 230 235 240
 Val Arg Thr Tyr Asp Thr Val Glu Phe Leu Ser Ala Asp Thr Lys Thr
 245 250 255
 Thr Thr Val Asn Val Glu Ser Lys Asp Asn Gly Lys Lys Thr Glu Val
 260 265 270
 Lys Ile Gly Ala Lys Thr Ser Val Ile Lys Glu Lys Asp Gly Lys Leu
 275 280 285
 Val Thr Gly Lys Asp Lys Gly Glu Asn Gly Ser Ser Thr Asp Glu Gly
 290 295 300
 Glu Gly Leu Val Thr Ala Lys Glu Val Ile Asp Ala Val Asn Lys Ala
 305 310 315 320
 Gly Trp Arg Met Lys Thr Thr Thr Ala Asn Gly Gln Thr Gly Gln Ala
 325 330 335
 Asp Lys Phe Glu Thr Val Thr Ser Gly Thr Asn Val Thr Phe Ala Ser
 340 345 350
 Gly Lys Gly Thr Thr Ala Thr Val Ser Lys Asp Asp Gln Gly Asn Ile
 355 360 365
 Thr Val Met Tyr Asp Val Asn Val Gly Asp Ala Leu Asn Val Asn Gln
 370 375 380
 Leu Gln Asn Ser Gly Trp Asn Leu Asp Ser Lys Ala Val Ala Gly Ser
 385 390 395 400
 Ser Gly Lys Val Ile Ser Gly Asn Val Ser Pro Ser Lys Gly Lys Met
 405 410 415
 Asp Glu Thr Val Asn Ile Asn Ala Gly Asn Asn Ile Glu Ile Thr Arg
 420 425 430

Asn Gly Lys Asn Ile Asp Ile Ala Thr Ser Met Thr Pro Gln Phe Ser
 435 440 445
 Ser Val Ser Leu Gly Ala Gly Ala Asp Ala Pro Thr Leu Ser Val Asp
 450 455 460
 Gly Asp Ala Leu Asn Val Gly Ser Lys Lys Asp Asn Lys Pro Val Arg
 465 470 475 480
 Ile Thr Asn Val Ala Pro Gly Val Lys Glu Gly Asp Val Thr Asn Val
 485 490 495
 Ala Gln Leu Lys Gly Val Ala Gln Asn Leu Asn Asn Arg Ile Asp Asn
 500 505 510
 Val Asp Gly Asn Ala Arg Ala Gly Ile Ala Gln Ala Ile Ala Thr Ala
 515 520 525
 Gly Leu Val Gln Ala Tyr Leu Pro Gly Lys Ser Met Met Ala Ile Gly
 530 535 540
 Gly Gly Thr Tyr Arg Gly Glu Ala Gly Tyr Ala Ile Gly Tyr Ser Ser
 545 550 555 560
 Ile Ser Asp Gly Gly Asn Trp Ile Ile Lys Gly Thr Ala Ser Gly Asn
 565 570 575
 Ser Arg Gly His Phe Gly Ala Ser Ala Ser Val Gly Tyr Gln Trp
 580 585 590

<210> 105
 <211> 591
 <212> PRT
 <213> Neisseria meningitidis

<400> 105
 Met Asn Lys Ile Tyr Arg Ile Ile Trp Asn Ser Ala Leu Asn Ala Trp
 1 5 10 15
 Val Val Val Ser Glu Leu Thr Arg Asn His Thr Lys Arg Ala Ser Ala
 20 25 30
 Thr Val Lys Thr Ala Val Leu Ala Thr Leu Leu Phe Ala Thr Val Gln
 35 40 45
 Ala Ser Ala Asn Asn Glu Glu Gln Glu Asp Leu Tyr Leu Asp Pro
 50 55 60
 Val Gln Arg Thr Val Ala Val Leu Ile Val Asn Ser Asp Lys Glu Gly
 65 70 75 80
 Thr Gly Glu Lys Glu Lys Val Glu Glu Asn Ser Asp Trp Ala Val Tyr
 85 90 95
 Phe Asn Glu Lys Gly Val Leu Thr Ala Arg Glu Ile Thr Leu Lys Ala

100					105					110					
Gly	Asp	Asn	Leu	Lys	Ile	Lys	Gln	Asn	Gly	Thr	Asn	Phe	Thr	Tyr	Ser
		115					120					125			
Leu	Lys	Lys	Asp	Leu	Thr	Asp	Leu	Thr	Ser	Val	Gly	Thr	Glu	Lys	Leu
		130					135					140			
Ser	Phe	Ser	Ala	Asn	Gly	Asn	Lys	Val	Asn	Ile	Thr	Ser	Asp	Thr	Lys
							150					155			
Gly	Leu	Asn	Phe	Ala	Lys	Glu	Thr	Ala	Gly	Thr	Asn	Gly	Asp	Thr	Thr
				165					170					175	
Val	His	Leu	Asn	Gly	Ile	Gly	Ser	Thr	Leu	Thr	Asp	Thr	Leu	Leu	Asn
			180					185					190		
Thr	Gly	Ala	Thr	Thr	Asn	Val	Thr	Asn	Asp	Asn	Val	Thr	Asp	Asp	Glu
			195					200					205		
Lys	Lys	Arg	Ala	Ala	Ser	Val	Lys	Asp	Val	Leu	Asn	Ala	Gly	Trp	Asn
			210				215					220			
Ile	Lys	Gly	Val	Lys	Pro	Gly	Thr	Thr	Ala	Ser	Asp	Asn	Val	Asp	Phe
							230					235			
Val	Arg	Thr	Tyr	Asp	Thr	Val	Glu	Phe	Leu	Ser	Ala	Asp	Thr	Lys	Thr
				245					250					255	
Thr	Thr	Val	Asn	Val	Glu	Ser	Lys	Asp	Asn	Gly	Lys	Lys	Thr	Glu	Val
			260					265					270		
Lys	Ile	Gly	Ala	Lys	Thr	Ser	Val	Ile	Lys	Glu	Lys	Asp	Gly	Lys	Leu
			275				280					285			
Val	Thr	Gly	Lys	Asp	Lys	Gly	Glu	Asn	Gly	Ser	Ser	Thr	Asp	Glu	Gly
			290				295					300			
Glu	Gly	Leu	Val	Thr	Ala	Lys	Glu	Val	Ile	Asp	Ala	Val	Asn	Lys	Ala
							310					315			
Gly	Trp	Arg	Met	Lys	Thr	Thr	Thr	Ala	Asn	Gly	Gln	Thr	Gly	Gln	Ala
				325					330					335	
Asp	Lys	Phe	Glu	Thr	Val	Thr	Ser	Gly	Thr	Asn	Val	Thr	Phe	Ala	Ser
			340					345					350		
Gly	Lys	Gly	Thr	Thr	Ala	Thr	Val	Ser	Lys	Asp	Asp	Gln	Gly	Asn	Ile
			355				360					365			
Thr	Val	Met	Tyr	Asp	Val	Asn	Val	Gly	Asp	Ala	Leu	Asn	Val	Asn	Gln
							375					380			
Leu	Gln	Asn	Ser	Gly	Trp	Asn	Leu	Asp	Ser	Lys	Ala	Val	Ala	Gly	Ser
							390					395			
Ser	Gly	Lys	Val	Ile	Ser	Gly	Asn	Val	Ser	Pro	Ser	Lys	Gly	Lys	Met

405					410					415					
Asp	Glu	Thr	Val	Asn	Ile	Asn	Ala	Gly	Asn	Asn	Ile	Glu	Ile	Thr	Arg
			420					425					430		
Asn	Gly	Lys	Asn	Ile	Asp	Ile	Ala	Thr	Ser	Met	Thr	Pro	Gln	Phe	Ser
		435					440					445			
Ser	Val	Ser	Leu	Gly	Ala	Gly	Ala	Asp	Ala	Pro	Thr	Leu	Ser	Val	Asp
		450					455					460			
Gly	Asp	Ala	Leu	Asn	Val	Gly	Ser	Lys	Lys	Asp	Asn	Lys	Pro	Val	Arg
465						470					475				480
Ile	Thr	Asn	Val	Ala	Pro	Gly	Val	Lys	Glu	Gly	Asp	Val	Thr	Asn	Val
				485					490					495	
Ala	Gln	Leu	Lys	Gly	Val	Ala	Gln	Asn	Leu	Asn	Asn	Arg	Ile	Asp	Asn
			500					505					510		
Val	Asp	Gly	Asn	Ala	Arg	Ala	Gly	Ile	Ala	Gln	Ala	Ile	Ala	Thr	Ala
		515					520					525			
Gly	Leu	Val	Gln	Ala	Tyr	Leu	Pro	Gly	Lys	Ser	Met	Met	Ala	Ile	Gly
	530					535					540				
Gly	Gly	Thr	Tyr	Arg	Gly	Glu	Ala	Gly	Tyr	Ala	Ile	Gly	Tyr	Ser	Ser
545						550					555				560
Ile	Ser	Asp	Gly	Gly	Asn	Trp	Ile	Ile	Lys	Gly	Thr	Ala	Ser	Gly	Asn
				565					570					575	
Ser	Arg	Gly	His	Phe	Gly	Ala	Ser	Ala	Ser	Val	Gly	Tyr	Gln	Trp	
			580					585					590		

<210> 106
 <211> 592
 <212> PRT
 <213> Neisseria meningitidis

<400> 106

Met	Asn	Lys	Ile	Tyr	Arg	Ile	Ile	Trp	Asn	Ser	Ala	Leu	Asn	Ala	Trp
1				5				10					15		
Val	Ala	Val	Ser	Glu	Leu	Thr	Arg	Asn	His	Thr	Lys	Arg	Ala	Ser	Ala
			20					25					30		
Thr	Val	Lys	Thr	Ala	Val	Leu	Ala	Thr	Leu	Leu	Phe	Ala	Thr	Val	Gln
		35					40					45			
Ala	Asn	Ala	Thr	Asp	Glu	Asp	Glu	Glu	Glu	Glu	Leu	Glu	Ser	Val	Gln
		50				55					60				
Arg	Ser	Val	Val	Gly	Ser	Ile	Gln	Ala	Ser	Met	Glu	Gly	Ser	Gly	Glu
65					70				75						80

Leu Gln Asn Ser Gly Trp Asn Leu Asp Ser Lys Ala Val Ala Gly Ser
 385 390 395 400
 Ser Gly Lys Val Ile Ser Gly Asn Val Ser Pro Ser Lys Gly Lys Met
 405 410 415
 Asp Glu Thr Val Asn Ile Asn Ala Gly Asn Asn Ile Glu Ile Ser Arg
 420 425 430
 Asn Gly Lys Asn Ile Asp Ile Ala Thr Ser Met Ala Pro Gln Phe Ser
 435 440 445
 Ser Val Ser Leu Gly Ala Gly Ala Asp Ala Pro Thr Leu Ser Val Asp
 450 455 460
 Asp Glu Gly Ala Leu Asn Val Gly Ser Lys Asp Ala Asn Lys Pro Val
 465 470 475 480
 Arg Ile Thr Asn Val Ala Pro Gly Val Lys Glu Gly Asp Val Thr Asn
 485 490 495
 Val Ala Gln Leu Lys Gly Val Ala Gln Asn Leu Asn Asn Arg Ile Asp
 500 505 510
 Asn Val Asp Gly Asn Ala Arg Ala Gly Ile Ala Gln Ala Ile Ala Thr
 515 520 525
 Ala Gly Leu Val Gln Ala Tyr Leu Pro Gly Lys Ser Met Met Ala Ile
 530 535 540
 Gly Gly Gly Thr Tyr Arg Gly Glu Ala Gly Tyr Ala Ile Gly Tyr Ser
 545 550 555 560
 Ser Ile Ser Asp Gly Gly Asn Trp Ile Ile Lys Gly Thr Ala Ser Gly
 565 570 575
 Asn Ser Arg Gly His Phe Gly Ala Ser Ala Ser Val Gly Tyr Gln Trp
 580 585 590

<210> 107
 <211> 592
 <212> PRT
 <213> Neisseria meningitidis

<400> 107
 Met Asn Lys Ile Tyr Arg Ile Ile Trp Asn Ser Ala Leu Asn Ala Trp
 1 5 10 15
 Val Ala Val Ser Glu Leu Thr Arg Asn His Thr Lys Arg Ala Ser Ala
 20 25 30
 Thr Val Lys Thr Ala Val Leu Ala Thr Leu Leu Phe Ala Thr Val Gln
 35 40 45

Ala Asn Ala Thr Asp Glu Asp Glu Glu Glu Glu Leu Glu Ser Val Gln
 50 55 60
 Arg Ser Val Val Gly Ser Ile Gln Ala Ser Met Glu Gly Ser Gly Glu
 65 70 75 80
 Leu Glu Thr Ile Ser Leu Ser Met Thr Asn Asp Ser Lys Glu Phe Val
 85 90 95
 Asp Pro Tyr Ile Val Val Thr Leu Lys Ala Gly Asp Asn Leu Lys Ile
 100 105 110
 Lys Gln Asn Thr Asn Glu Asn Thr Asn Ala Ser Ser Phe Thr Tyr Ser
 115 120 125
 Leu Lys Lys Asp Leu Thr Gly Leu Ile Asn Val Glu Thr Glu Lys Leu
 130 135 140
 Ser Phe Gly Ala Asn Gly Lys Lys Val Asn Ile Ile Ser Asp Thr Lys
 145 150 155 160
 Gly Leu Asn Phe Ala Lys Glu Thr Ala Gly Thr Asn Gly Asp Thr Thr
 165 170 175
 Val His Leu Asn Gly Ile Gly Ser Thr Leu Thr Asp Thr Leu Ala Gly
 180 185 190
 Ser Ser Ala Ser His Val Asp Ala Gly Asn Gln Ser Thr His Tyr Thr
 195 200 205
 Arg Ala Ala Ser Ile Lys Asp Val Leu Asn Ala Gly Trp Asn Ile Lys
 210 215 220
 Gly Val Lys Thr Gly Ser Thr Thr Gly Gln Ser Glu Asn Val Asp Phe
 225 230 235 240
 Val Arg Thr Tyr Asp Thr Val Glu Phe Leu Ser Ala Asp Thr Lys Thr
 245 250 255
 Thr Thr Val Asn Val Glu Ser Lys Asp Asn Gly Lys Arg Thr Glu Val
 260 265 270
 Lys Ile Gly Ala Lys Thr Ser Val Ile Lys Glu Lys Asp Gly Lys Leu
 275 280 285
 Val Thr Gly Lys Gly Lys Gly Glu Asn Gly Ser Ser Thr Asp Glu Gly
 290 295 300
 Glu Gly Leu Val Thr Ala Lys Glu Val Ile Asp Ala Val Asn Lys Ala
 305 310 315 320
 Gly Trp Arg Met Lys Thr Thr Thr Ala Asn Gly Gln Thr Gly Gln Ala
 325 330 335
 Asp Lys Phe Glu Thr Val Thr Ser Gly Thr Asn Val Thr Phe Ala Ser
 340 345 350

Gly Lys Gly Thr Thr Ala Thr Val Ser Lys Asp Asp Gln Gly Asn Ile
 355 360 365
 Thr Val Met Tyr Asp Val Asn Val Gly Asp Ala Leu Asn Val Asn Gln
 370 375 380
 Leu Gln Asn Ser Gly Trp Asn Leu Asp Ser Lys Ala Val Ala Gly Ser
 385 390 395 400
 Ser Gly Lys Val Ile Ser Gly Asn Val Ser Pro Ser Lys Gly Lys Met
 405 410 415
 Asp Glu Thr Val Asn Ile Asn Ala Gly Asn Asn Ile Glu Ile Ser Arg
 420 425 430
 Asn Gly Lys Asn Ile Asp Ile Ala Thr Ser Met Ala Pro Gln Phe Ser
 435 440 445
 Ser Val Ser Leu Gly Ala Gly Ala Asp Ala Pro Thr Leu Ser Val Asp
 450 455 460
 Asp Glu Gly Ala Leu Asn Val Gly Ser Lys Asp Ala Asn Lys Pro Val
 465 470 475 480
 Arg Ile Thr Asn Val Ala Pro Gly Val Lys Glu Gly Asp Val Thr Asn
 485 490 495
 Val Ala Gln Leu Lys Gly Val Ala Gln Asn Leu Asn Asn Arg Ile Asp
 500 505 510
 Asn Val Asp Gly Asn Ala Arg Ala Gly Ile Ala Gln Ala Ile Ala Thr
 515 520 525
 Ala Gly Leu Val Gln Ala Tyr Leu Pro Gly Lys Ser Met Met Ala Ile
 530 535 540
 Gly Gly Gly Thr Tyr Arg Gly Glu Ala Gly Tyr Ala Ile Gly Tyr Ser
 545 550 555 560
 Ser Ile Ser Asp Gly Gly Asn Trp Ile Ile Lys Gly Thr Ala Ser Gly
 565 570 575
 Asn Ser Arg Gly His Phe Gly Ala Ser Ala Ser Val Gly Tyr Gln Trp
 580 585 590

<210> 108
 <211> 589
 <212> PRT
 <213> Neisseria meningitidis

<400> 108
 Met Asn Lys Ile Tyr Arg Ile Ile Trp Asn Ser Ala Leu Asn Ala Trp

1	5	10	15
Val Val Val Ser Glu Leu Thr Arg Asn His Thr Lys Arg Ala Ser Ala	20	25	30
Thr Val Ala Thr Ala Val Leu Ala Thr Leu Leu Ser Ala Thr Val Gln	35	40	45
Ala Asn Ala Thr Asp Thr Asp Glu Asp Glu Glu Leu Glu Ser Val Val	50	55	60
Arg Ser Ala Leu Val Leu Gln Phe Met Ile Asp Lys Glu Gly Asn Gly	65	70	75
Glu Ile Glu Ser Thr Gly Asp Ile Gly Trp Ser Ile Tyr Tyr Asp Asp	85	90	95
His Asn Thr Leu His Gly Ala Thr Val Thr Leu Lys Ala Gly Asp Asn	100	105	110
Leu Lys Ile Lys Gln Ser Gly Lys Asp Phe Thr Tyr Ser Leu Lys Lys	115	120	125
Glu Leu Lys Asp Leu Thr Ser Val Glu Thr Glu Lys Leu Ser Phe Gly	130	135	140
Ala Asn Gly Asn Lys Val Asn Ile Thr Ser Asp Thr Lys Gly Leu Asn	145	150	155
Phe Ala Lys Glu Thr Ala Gly Thr Asn Gly Asp Pro Thr Val His Leu	165	170	175
Asn Gly Ile Gly Ser Thr Leu Thr Asp Thr Leu Ala Gly Ser Ser Ala	180	185	190
Ser His Val Asp Ala Gly Asn Gln Ser Thr His Tyr Thr Arg Ala Ala	195	200	205
Ser Ile Lys Asp Val Leu Asn Ala Gly Trp Asn Ile Lys Gly Val Lys	210	215	220
Thr Gly Ser Thr Thr Gly Gln Ser Glu Asn Val Asp Phe Val Arg Thr	225	230	235
Tyr Asp Thr Val Glu Phe Leu Ser Ala Asp Thr Lys Thr Thr Thr Val	245	250	255
Asn Val Glu Ser Lys Asp Asn Gly Lys Arg Thr Glu Val Lys Ile Gly	260	265	270
Ala Lys Thr Ser Val Ile Lys Glu Lys Asp Gly Lys Leu Val Thr Gly	275	280	285
Lys Gly Lys Gly Glu Asn Gly Ser Ser Thr Asp Glu Gly Glu Gly Leu	290	295	300
Val Thr Ala Lys Glu Val Ile Asp Ala Val Asn Lys Ala Gly Trp Arg			

305		310		315		320									
Met	Lys	Thr	Thr	Thr	Ala	Asn	Gly	Gln	Thr	Gly	Gln	Ala	Asp	Lys	Phe
				325					330					335	
Glu	Thr	Val	Thr	Ser	Gly	Thr	Lys	Val	Thr	Phe	Ala	Ser	Gly	Asn	Gly
			340					345					350		
Thr	Thr	Ala	Thr	Val	Ser	Lys	Asp	Asp	Gln	Gly	Asn	Ile	Thr	Val	Lys
		355					360					365			
Tyr	Asp	Val	Asn	Val	Gly	Asp	Ala	Leu	Asn	Val	Asn	Gln	Leu	Gln	Asn
	370					375					380				
Ser	Gly	Trp	Asn	Leu	Asp	Ser	Lys	Ala	Val	Ala	Gly	Ser	Ser	Gly	Lys
385					390					395					400
Val	Ile	Ser	Gly	Asn	Val	Ser	Pro	Ser	Lys	Gly	Lys	Met	Asp	Glu	Thr
			405						410					415	
Val	Asn	Ile	Asn	Ala	Gly	Asn	Asn	Ile	Glu	Ile	Thr	Arg	Asn	Gly	Lys
			420					425					430		
Asn	Ile	Asp	Ile	Ala	Thr	Ser	Met	Thr	Pro	Gln	Phe	Ser	Ser	Val	Ser
		435					440					445			
Leu	Gly	Ala	Gly	Ala	Asp	Ala	Pro	Thr	Leu	Ser	Val	Asp	Asp	Glu	Gly
	450					455					460				
Ala	Leu	Asn	Val	Gly	Ser	Lys	Asp	Ala	Asn	Lys	Pro	Val	Arg	Ile	Thr
465					470					475					480
Asn	Val	Ala	Pro	Gly	Val	Lys	Glu	Gly	Asp	Val	Thr	Asn	Val	Ala	Gln
			485					490						495	
Leu	Lys	Gly	Val	Ala	Gln	Asn	Leu	Asn	Asn	Arg	Ile	Asp	Asn	Val	Asp
			500				505						510		
Gly	Asn	Ala	Arg	Ala	Gly	Ile	Ala	Gln	Ala	Ile	Ala	Thr	Ala	Gly	Leu
	515						520					525			
Ala	Gln	Ala	Tyr	Leu	Pro	Gly	Lys	Ser	Met	Met	Ala	Ile	Gly	Gly	Gly
	530					535					540				
Thr	Tyr	Arg	Gly	Glu	Ala	Gly	Tyr	Ala	Ile	Gly	Tyr	Ser	Ser	Ile	Ser
545					550					555					560
Asp	Thr	Gly	Asn	Trp	Val	Ile	Lys	Gly	Thr	Ala	Ser	Gly	Asn	Ser	Arg
			565						570					575	
Gly	His	Phe	Gly	Thr	Ser	Ala	Ser	Val	Gly	Tyr	Gln	Trp			
			580					585							

<210> 109
 <211> 589
 <212> PRT

<213> Neisseria meningitidis

<400> 109

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Met Asn Lys Ile Tyr Arg Ile Ile Trp Asn Ser Ala Leu Asn Ala Trp
 1           5           10           15

Val Val Val Ser Glu Leu Thr Arg Asn His Thr Lys Arg Ala Ser Ala
      20           25           30

Thr Val Ala Thr Ala Val' Leu Ala Thr Leu Leu Ser Ala Thr Val Gln
 35           40           45

Ala Asn Ala Thr Asp Thr Asp Glu Asp Glu Glu Leu Glu Ser Val Val
 50           55           60

Arg Ser Ala Leu Val Leu Gln Phe Met Ile Asp Lys Glu Gly Asn Gly
 65           70           75           80

Glu Ile Glu Ser Thr Gly Asp Ile Gly Trp Ser Ile Tyr Tyr Asp Asp
      85           90           95

His Asn Thr Leu His Gly Ala Thr Val Thr Leu Lys Ala Gly Asp Asn
      100           105           110

Leu Lys Ile Lys Gln Ser Gly Lys Asp Phe Thr Tyr Ser Leu Lys Lys
      115           120           125

Glu Leu Lys Asp Leu Thr Ser Val Glu Thr Glu Lys Leu Ser Phe Gly
      130           135           140

Ala Asn Gly Asn Lys Val Asn Ile Thr Ser Asp Thr Lys Gly Leu Asn
      145           150           155           160

Phe Ala Lys Glu Thr Ala Gly Thr Asn Gly Asp Pro Thr Val His Leu
      165           170           175

Asn Gly Ile Gly Ser Thr Leu Thr Asp Thr Leu Ala Gly Ser Ser Ala
      180           185           190

Ser His Val Asp Ala Gly Asn Gln Ser Thr His Tyr Thr Arg Ala Ala
      195           200           205

Ser Ile Lys Asp Val Leu Asn Ala Gly Trp Asn Ile Lys Gly Val Lys
      210           215           220

Thr Gly Ser Thr Thr Gly Gln Ser Glu Asn Val Asp Phe Val Arg Thr
      225           230           235           240

Tyr Asp Thr Val Glu Phe Leu Ser Ala Asp Thr Lys Thr Thr Thr Val
      245           250           255

Asn Val Glu Ser Lys Asp Asn Gly Lys Arg Thr Glu Val Lys Ile Gly
      260           265           270

Ala Lys Thr Ser Val Ile Lys Glu Lys Asp Gly Lys Leu Val Thr Gly
      275           280           285

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Lys Gly Lys Gly Glu Asn Gly Ser Ser Thr Asp Glu Gly Glu Gly Leu
 290 295 300
 Val Thr Ala Lys Glu Val Ile Asp Ala Val Asn Lys Ala Gly Trp Arg
 305 310 315 320
 Met Lys Thr Thr Thr Ala Asn Gly Gln Thr Gly Gln Ala Asp Lys Phe
 325 330 335
 Glu Thr Val Thr Ser Gly Thr Lys Val Thr Phe Ala Ser Gly Asn Gly
 340 345 350
 Thr Thr Ala Thr Val Ser Lys Asp Asp Gln Gly Asn Ile Thr Val Lys
 355 360 365
 Tyr Asp Val Asn Val Gly Asp Ala Leu Asn Val Asn Gln Leu Gln Asn
 370 375 380
 Ser Gly Trp Asn Leu Asp Ser Lys Ala Val Ala Gly Ser Ser Gly Lys
 385 390 395 400
 Val Ile Ser Gly Asn Val Ser Pro Ser Lys Gly Lys Met Asp Glu Thr
 405 410 415
 Val Asn Ile Asn Ala Gly Asn Asn Ile Glu Ile Thr Arg Asn Gly Lys
 420 425 430
 Asn Ile Asp Ile Ala Thr Ser Met Thr Pro Gln Phe Ser Ser Val Ser
 435 440 445
 Leu Gly Ala Gly Ala Asp Ala Pro Thr Leu Ser Val Asp Asp Glu Gly
 450 455 460
 Ala Leu Asn Val Gly Ser Lys Asp Ala Asn Lys Pro Val Arg Ile Thr
 465 470 475 480
 Asn Val Ala Pro Gly Val Lys Glu Gly Asp Val Thr Asn Val Ala Gln
 485 490 495
 Leu Lys Gly Val Ala Gln Asn Leu Asn Asn Arg Ile Asp Asn Val Asp
 500 505 510
 Gly Asn Ala Arg Ala Gly Ile Ala Gln Ala Ile Ala Thr Ala Gly Leu
 515 520 525
 Ala Gln Ala Tyr Leu Pro Gly Lys Ser Met Met Ala Ile Gly Gly Gly
 530 535 540
 Thr Tyr Arg Gly Glu Ala Gly Tyr Ala Ile Gly Tyr Ser Ser Ile Ser
 545 550 555 560
 Asp Thr Gly Asn Trp Val Ile Lys Gly Thr Ala Ser Gly Asn Ser Arg
 565 570 575
 Gly His Phe Gly Thr Ser Ala Ser Val Gly Tyr Gln Trp
 580 585

<210> 110
 <211> 592
 <212> PRT
 <213> Neisseria meningitidis

<400> 110

Met	Asn	Lys	Ile	Tyr	Arg	Ile	Ile	Trp	Asn	Ser	Ala	Leu	Asn	Ala	Trp
1				5					10					15	
Val	Ala	Val	Ser	Glu	Leu	Thr	Arg	Asn	His	Thr	Lys	Arg	Ala	Ser	Ala
			20					25					30		
Thr	Val	Lys	Thr	Ala	Val	Leu	Ala	Thr	Leu	Leu	Phe	Ala	Thr	Val	Gln
		35					40					45			
Ala	Asn	Ala	Thr	Asp	Glu	Asp	Glu	Glu	Glu	Glu	Leu	Glu	Ser	Val	Gln
	50					55					60				
Arg	Ser	Val	Val	Gly	Ser	Ile	Gln	Ala	Ser	Met	Glu	Gly	Ser	Gly	Glu
65					70					75					80
Leu	Glu	Thr	Ile	Ser	Leu	Ser	Met	Thr	Asn	Asp	Ser	Lys	Glu	Phe	Val
				85					90					95	
Asp	Pro	Tyr	Ile	Val	Val	Thr	Leu	Lys	Ala	Gly	Asp	Asn	Leu	Lys	Ile
			100					105					110		
Lys	Gln	Asn	Thr	Asn	Glu	Asn	Thr	Asn	Ala	Ser	Ser	Phe	Thr	Tyr	Ser
		115					120					125			
Leu	Lys	Lys	Asp	Leu	Thr	Gly	Leu	Ile	Asn	Val	Glu	Thr	Glu	Lys	Leu
	130					135					140				
Ser	Phe	Gly	Ala	Asn	Gly	Lys	Lys	Val	Asn	Ile	Ile	Ser	Asp	Thr	Lys
145					150					155					160
Gly	Leu	Asn	Phe	Ala	Lys	Glu	Thr	Ala	Gly	Thr	Asn	Gly	Asp	Thr	Thr
			165						170					175	
Val	His	Leu	Asn	Gly	Ile	Gly	Ser	Thr	Leu	Thr	Asp	Met	Leu	Leu	Asn
			180					185					190		
Thr	Gly	Ala	Thr	Thr	Asn	Val	Thr	Asn	Asp	Asn	Val	Thr	Asp	Asp	Glu
		195				200						205			
Lys	Lys	Arg	Ala	Ala	Ser	Val	Lys	Asp	Val	Leu	Asn	Ala	Gly	Trp	Asn
	210					215					220				
Ile	Lys	Gly	Val	Lys	Pro	Gly	Thr	Thr	Ala	Ser	Asp	Asn	Val	Asp	Phe
225					230					235					240
Val	Arg	Thr	Tyr	Asp	Thr	Val	Glu	Phe	Leu	Ser	Ala	Asp	Thr	Lys	Thr
			245						250					255	
Thr	Thr	Val	Asn	Val	Glu	Ser	Lys	Asp	Asn	Gly	Lys	Lys	Thr	Glu	Val
			260					265					270		

Lys Ile Gly Ala Lys Thr Ser Val Ile Lys Glu Lys Asp Gly Lys Leu
 275 280 285
 Val Thr Gly Lys Gly Lys Gly Glu Asn Gly Ser Ser Thr Asp Glu Gly
 290 295 300
 Glu Gly Leu Val Thr Ala Lys Glu Val Ile Asp Ala Val Asn Lys Ala
 305 310 315 320
 Gly Trp Arg Met Lys Thr Thr Thr Ala Asn Gly Gln Thr Gly Gln Ala
 325 330 335
 Asp Lys Phe Glu Thr Val Thr Ser Gly Thr Asn Val Thr Phe Ala Ser
 340 345 350
 Gly Lys Gly Thr Thr Ala Thr Val Ser Lys Asp Asp Gln Gly Asn Ile
 355 360 365
 Thr Val Met Tyr Asp Val Asn Val Gly Asp Ala Leu Asn Val Asn Gln
 370 375 380
 Leu Gln Asn Ser Gly Trp Asn Leu Asp Ser Lys Ala Val Ala Gly Ser
 385 390 395 400
 Ser Gly Lys Val Ile Ser Gly Asn Val Ser Pro Ser Lys Gly Lys Met
 405 410 415
 Asp Glu Thr Val Asn Ile Asn Ala Gly Asn Asn Ile Glu Ile Thr Arg
 420 425 430
 Asn Gly Lys Asn Ile Asp Ile Ala Thr Ser Met Thr Pro Gln Phe Ser
 435 440 445
 Ser Val Ser Leu Gly Ala Gly Ala Asp Ala Pro Thr Leu Ser Val Asp
 450 455 460
 Asp Lys Gly Ala Leu Asn Val Gly Ser Lys Asp Ala Asn Lys Pro Val
 465 470 475 480
 Arg Ile Thr Asn Val Ala Pro Gly Val Lys Glu Gly Asp Val Thr Asn
 485 490 495
 Val Ala Gln Leu Lys Gly Val Ala Gln Asn Leu Asn Asn Arg Ile Asp
 500 505 510
 Asn Val Asp Gly Asn Ala Arg Ala Gly Ile Ala Gln Ala Ile Ala Thr
 515 520 525
 Ala Gly Leu Val Gln Ala Tyr Leu Pro Gly Lys Ser Met Met Ala Ile
 530 535 540
 Gly Gly Gly Thr Tyr Arg Gly Glu Ala Gly Tyr Ala Ile Gly Tyr Ser
 545 550 555 560
 Ser Ile Ser Asp Gly Gly Asn Trp Ile Ile Lys Gly Thr Ala Ser Gly
 565 570 575

Asn Ser Arg Gly His Phe Gly Ala Ser Ala Ser Val Gly Tyr Gln Trp
580 585 590

<210> 111
<211> 600
<212> PRT
<213> Neisseria meningitidis

<400> 111
Met Asn Lys Ile Tyr Arg Ile Ile Trp Asn Ile Ala Leu Asn Ala Trp
1 5 10 15
Val Val Val Ser Glu Leu Thr Arg Asn His Thr Lys Arg Ala Ser Ala
20 25 30
Thr Val Ala Thr Ala Val Leu Ala Thr Leu Leu Ser Ala Thr Val Gln
35 40 45
Ala Asn Ala Thr Asp Glu Glu Asp Asn Glu Asp Leu Glu Pro Val Val
50 55 60
Arg Thr Ala Pro Val Leu Ser Phe His Ser Asp Lys Glu Gly Thr Gly
65 70 75 80
Glu Lys Glu Glu Val Gly Ala Ser Ser Asn Leu Thr Val Tyr Phe Asp
85 90 95
Lys Asn Arg Val Leu Lys Ala Gly Thr Ile Thr Leu Lys Ala Gly Asp
100 105 110
Asn Leu Lys Ile Lys Gln Asn Thr Asn Glu Asn Thr Asn Glu Asn Thr
115 120 125
Asn Ala Ser Ser Phe Thr Tyr Ser Leu Lys Lys Asp Leu Thr Gly Leu
130 135 140
Ile Asn Val Glu Thr Glu Lys Leu Ser Phe Gly Ala Asn Gly Lys Lys
145 150 155 160
Val Asn Ile Ile Ser Asp Thr Lys Gly Leu Asn Phe Ala Lys Glu Thr
165 170 175
Ala Gly Thr Asn Gly Asp Pro Thr Val His Leu Asn Gly Ile Gly Ser
180 185 190
Thr Leu Thr Asp Thr Leu Ala Gly Ser Ser Ala Ser His Val Asp Ala
195 200 205
Gly Asn Gln Ser Thr His Tyr Thr Arg Ala Ala Ser Ile Lys Asp Val
210 215 220
Leu Asn Ala Gly Trp Asn Ile Lys Gly Val Lys Thr Gly Ser Thr Thr

225		230		235		240
Gly Gln Ser Glu Asn Val Asp Phe Val Arg Thr Tyr Asp Thr Val Glu						
	245			250		255
Phe Leu Ser Ala Asp Thr Lys Thr Thr Thr Val Asn Val Glu Ser Lys						
	260			265		270
Asp Asn Gly Lys Arg Thr Glu Val Lys Ile Gly Ala Lys Thr Ser Val						
	275			280		285
Ile Lys Glu Lys Asp Gly Lys Leu Val Thr Gly Lys Gly Lys Gly Glu						
	290			295		300
Asn Gly Ser Ser Thr Asp Glu Gly Glu Gly Leu Val Thr Ala Lys Glu						
305		310		315		320
Val Ile Asp Ala Val Asn Lys Ala Gly Trp Arg Met Lys Thr Thr Thr						
	325			330		335
Ala Asn Gly Gln Thr Gly Gln Ala Asp Lys Phe Glu Thr Val Thr Ser						
	340			345		350
Gly Thr Lys Val Thr Phe Ala Ser Gly Asn Gly Thr Thr Ala Thr Val						
	355			360		365
Ser Lys Asp Asp Gln Gly Asn Ile Thr Val Lys Tyr Asp Val Asn Val						
	370			375		380
Gly Asp Ala Leu Asn Val Asn Gln Leu Gln Asn Ser Gly Trp Asn Leu						
385		390		395		400
Asp Ser Lys Ala Val Ala Gly Ser Ser Gly Lys Val Ile Ser Gly Asn						
	405			410		415
Val Ser Pro Ser Lys Gly Lys Met Asp Glu Thr Val Asn Ile Asn Ala						
	420			425		430
Gly Asn Asn Ile Glu Ile Thr Arg Asn Gly Lys Asn Ile Asp Ile Ala						
	435			440		445
Thr Ser Met Thr Pro Gln Phe Ser Ser Val Ser Leu Gly Ala Gly Ala						
	450			455		460
Asp Ala Pro Thr Leu Ser Val Asp Asp Glu Gly Ala Leu Asn Val Gly						
465		470		475		480
Ser Lys Asp Ala Asn Lys Pro Val Arg Ile Thr Asn Val Ala Pro Gly						
	485			490		495
Val Lys Glu Gly Asp Val Thr Asn Val Ala Gln Leu Lys Gly Val Ala						
	500			505		510
Gln Asn Leu Asn Asn Arg Ile Asp Asn Val Asp Gly Asn Ala Arg Ala						
	515			520		525
Gly Ile Ala Gln Ala Ile Ala Thr Ala Gly Leu Val Gln Ala Tyr Leu						

530	535	540
Pro Gly Lys Ser Met Met Ala Ile Gly Gly Gly Thr Tyr Arg Gly Glu		
545	550	555 560
Ala Gly Tyr Ala Ile Gly Tyr Ser Ser Ile Ser Asp Gly Gly Asn Trp		
	565	570 575
Ile Ile Lys Gly Thr Ala Ser Gly Asn Ser Arg Gly His Phe Gly Ala		
	580	585 590
Ser Ala Ser Val Gly Tyr Gln Trp		
	595	600

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<400> 112
 cgcggatccc atatgtcgcc gcaaaattcc ga 32

<210> 113
 <211> 28
 <212> DNA
 <213> Neisseria meningitidis

<400> 113
 cccgctcgag ttttgccgcg ttaaaagc 28

<210> 114
 <211> 30
 <212> DNA
 <213> Neisseria meningitidis

<400> 114
 cgcggatccc atatgaccgt gaagaccgcc 30

<210> 115
 <211> 28
 <212> DNA
 <213> Neisseria meningitidis

<400> 115
 cccgctcgag ccaactgataa ccgacaga 28

<210> 116
 <211> 34
 <212> DNA
 <213> Neisseria meningitidis

<400> 116

cgcggatccc atatgtatTTT gaaacagctc caag	34
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<p><400> 117 cccgctcgag ttctgggtga atgtta</p>	26
<p><210> 118 <211> 29 <212> DNA <213> Neisseria meningitidis</p>	
<p><400> 118 gcggatccca tatgggcacg gacaacccc</p>	29
<p><210> 119 <211> 26 <212> DNA <213> Neisseria meningitidis</p>	
<p><400> 119 cccgctcgag acgtggggaa cagtct</p>	26
<p><210> 120 <211> 34 <212> DNA <213> Neisseria meningitidis</p>	
<p><400> 120 gcggatccca tatgaaaaat attcaagtag ttgc</p>	34
<p><210> 121 <211> 27 <212> DNA <213> Neisseria meningitidis</p>	
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<p><210> 122 <211> 31 <212> DNA <213> Neisseria meningitidis</p>	
<p><400> 122 cgcggatccc atatgtgcca accgcaatcc g</p>	31

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 <400> 123
 cccgctcgag tttttccagc tccggca 27

 <210> 124
 <211> 33
 <212> DNA
 <213> *Neisseria meningitidis*

 <400> 124
 gcggatccca tatggttata ggaatattac tcg 33

 <210> 125
 <211> 25
 <212> DNA
 <213> *Neisseria meningitidis*

 <400> 125
 cccgctcgag ggctgcagaa gctgg 25

 <210> 126
 <211> 32
 <212> DNA
 <213> *Neisseria meningitidis*

 <400> 126
 cgcgatccc atatgcggac gtggttggtt tt 32

 <210> 127
 <211> 30
 <212> DNA
 <213> *Neisseria meningitidis*

 <400> 127
 cccgctcgag atatcttcg tttttttcac 30

 <210> 128
 <211> 36
 <212> DNA
 <213> *Neisseria meningitidis*

 <400> 128
 cgcgatccg ctagcgtaaa tttattattt ttagaa 36

 <210> 129
 <211> 28
 <212> DNA

<213> Neisseria meningitidis
 <400> 129
 cccgctcgag ttccaactca ttgaagta 28
 <210> 130
 <211> 35
 <212> DNA
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 <400> 130
 cgcggtatccc atatgaataa aggtttacat cgcac 35
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 <211> 26
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 <400> 131
 cccgctcgag aatcgctgca ccggct 26
 <210> 132
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 <400> 132
 cgcggtatccc atatgactgc cttttcgaca 30
 <210> 133
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 <400> 133
 cccgctcgag gcgtgaagcg tcagga 26
 <210> 134
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 <223> Description of Artificial Sequence: BamHI - NdeI
 <400> 134
 cgcggtatccc atatg 15
 <210> 135
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<220>
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 <400> 135
 cgcggatccg ctagc 15

 <210> 136
 <211> 17
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 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: EcoRI - NheI

 <400> 136
 ccggaattct agctagc 17

 <210> 137
 <211> 10
 <212> DNA
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 <220>
 <223> Description of Artificial Sequence: XhoI

 <400> 137
 cccgctcgag 10

 <210> 138
 <211> 291
 <212> PRT
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 <220>
 <223> Description of Artificial Sequence: ORF40a

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 <400> 138
 Ser Ala Leu Asn Ala Xaa Val Ala Val Ser Glu Leu Thr Arg Asn His
 1 5 10 15
 Thr Lys Arg Ala Ser Ala Thr Val Lys Thr Ala Val Leu Ala Thr Leu
 20 25 30
 Leu Phe Ala Thr Val Gln Ala Asn Ala Thr Asp Glu Asp Glu Glu Glu
 35 40 45
 Glu Leu Glu Ser Val Gln Arg Ser Val Val Gly Ser Ile Gln Ala Ser
 50 55 60
 Met Glu Gly Ser Gly Glu Leu Glu Thr Ile Ser Leu Ser Met Thr Asn
 65 70 75 80
 Asp Ser Lys Glu Phe Val Asp Pro Tyr Ile Val Val Thr Leu Lys Ala
 85 90 95
 Gly Asp Asn Leu Lys Ile Lys Gln Asn Thr Asn Glu Asn Thr Asn Ala
 100 105 110
 Ser Ser Phe Thr Tyr Ser Leu Lys Lys Asp Leu Thr Gly Leu Ile Asn
 115 120 125
 Val Xaa Thr Glu Lys Leu Ser Phe Gly Ala Asn Gly Lys Lys Val Asn
 130 135 140
 Ile Ile Ser Asp Thr Lys Gly Leu Asn Phe Ala Lys Glu Thr Ala Gly
 145 150 155 160
 Thr Asn Gly Asp Thr Thr Val His Leu Asn Gly Ile Gly Ser Thr Leu
 165 170 175
 Thr Asp Thr Leu Ala Gly Ser Ser Ala Ser His Val Asp Ala Gly Asn
 180 185 190
 Xaa Ser Thr His Tyr Thr Arg Ala Ala Ser Ile Lys Asp Val Leu Asn
 195 200 205
 Ala Gly Trp Asn Ile Lys Gly Val Lys Xaa Gly Ser Thr Thr Gly Gln
 210 215 220
 Ser Glu Asn Val Asp Phe Val Arg Thr Tyr Asp Thr Val Glu Phe Leu
 225 230 235 240
 Ser Ala Asp Thr Xaa Thr Thr Thr Val Asn Val Glu Ser Lys Asp Asn
 245 250 255
 Gly Lys Arg Thr Glu Val Lys Ile Gly Ala Lys Thr Ser Val Ile Lys
 260 265 270

Glu Lys Asp Gly Lys Leu Val Thr Gly Lys Gly Lys Gly Glu Asn Gly
 275 280 285

Ser Ser Thr
 290

<210> 139
 <211> 240
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Hsf

<400> 139
 Thr Leu Leu Phe Ala Thr Val Gln Ala Asn Ala Thr Asp Glu Asp Glu
 1 5 10 15
 Glu Leu Asp Pro Val Val Arg Thr Ala Pro Val Leu Ser Phe His Ser
 20 25 30
 Asp Lys Glu Gly Thr Gly Glu Lys Glu Val Thr Glu Asn Ser Asn Trp
 35 40 45
 Gly Ile Tyr Phe Asp Asn Lys Gly Val Leu Lys Ala Gly Ala Ile Thr
 50 55 60
 Leu Lys Ala Gly Asp Asn Leu Lys Ile Lys Gln Asn Thr Asp Glu Ser
 65 70 75 80
 Thr Asn Ala Ser Ser Phe Thr Tyr Ser Leu Lys Lys Asp Leu Thr Asp
 85 90 95
 Leu Thr Ser Val Ala Thr Glu Lys Leu Ser Phe Gly Ala Asn Gly Asp
 100 105 110
 Lys Val Asp Ile Thr Ser Asp Ala Asn Gly Leu Lys Leu Ala Lys Thr
 115 120 125
 Gly Asn Gly Asn Val His Leu Asn Gly Leu Asp Ser Thr Leu Pro Asp
 130 135 140
 Ala Val Thr Asn Thr Gly Val Leu Ser Ser Ser Ser Phe Thr Pro Asn
 145 150 155 160
 Asp Val Glu Lys Thr Arg Ala Ala Thr Val Lys Asp Val Leu Asn Ala
 165 170 175
 Gly Trp Asn Ile Lys Gly Ala Lys Thr Ala Gly Gly Asn Val Glu Ser
 180 185 190
 Val Asp Leu Val Ser Ala Tyr Asn Asn Val Glu Phe Ile Thr Gly Asp
 195 200 205
 Lys Asn Thr Leu Asp Val Val Leu Thr Ala Lys Glu Asn Gly Lys Thr
 210 215 220

Thr	Glu	Val	Lys	Phe	Thr	Pro	Lys	Thr	Ser	Val	Ile	Lys	Glu	Lys	Asp
225					230					235					240

<210> 140

<211> 251

<212> PRT

<213> Artificial Sequence .

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<223> Description of Artificial Sequence: overlap identity

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<223> absent or positive

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<221> SITE

<222> (12)..(13)

<223> absent or positive

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<223> absent or positive

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<223> absent or positive

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<223> absent or positive

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<223> absent or positive

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<223> absent or positive

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<222> (133)..(138)
<223> absent or positive

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<223> absent or positive

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 <222> (231)
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 <222> (235)
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<220>
 <221> SITE
 <222> (240)..(242)
 <223> absent or positive

<400> 140
 Thr Leu Leu Phe Ala Thr Val Gln Ala Xaa Ala Xaa Xaa Glu Xaa Xaa
 1 5 10 15
 Glu Xaa Xaa Xaa Xaa Leu Asp Pro Val Xaa Arg Thr Xaa Xaa Val Leu
 20 25 30
 Xaa Xaa Xaa Ser Asp Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 35 40 45

Xaa Asn Ser Xaa Trp Xaa Xaa Tyr Phe Xaa Xaa Lys Gly Val Leu Xaa
50 55 60
Ala Xaa Xaa Ile Thr Xaa Lys Ala Gly Asp Asn Leu Lys Ile Lys Gln
65 70 75 80
Asn Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Phe Thr Tyr Ser Leu Lys
85 90 95
Lys Asp Leu Thr Asp Leu Thr Ser Val Xaa Thr Glu Lys Leu Ser Phe
100 105 110
Xaa Ala Asn Gly Xaa Lys Val Xaa Ile Thr Ser Asp Xaa Xaa Gly Leu
115 120 125
Xaa Xaa Ala Lys Xaa Xaa Xaa Xaa Xaa Xaa Gly Xaa Xaa Xaa Val His
130 135 140
Leu Asn Gly Xaa Xaa Ser Thr Leu Xaa Asp Xaa Xaa Xaa Asn Thr Gly
145 150 155 160
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Glu Lys Xaa
165 170 175
Arg Ala Ala Xaa Val Lys Asp Val Leu Asn Ala Gly Trp Asn Ile Lys
180 185 190
Gly Xaa Lys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Val Asp Xaa Val Xaa
195 200 205
Xaa Tyr Xaa Xaa Val Glu Phe Xaa Xaa Xaa Asp Xaa Xaa Thr Xaa Xaa
210 215 220
Val Xaa Xaa Xaa Xaa Lys Xaa Asn Gly Lys Xaa Thr Glu Val Lys Xaa
225 230 235 240
Xaa Xaa Lys Thr Ser Val Ile Lys Glu Lys Asp
245 250

<210> 141

<211> 36

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: ORF40a

<400> 141

Val Ala Val Ser Glu Leu Thr Arg Asn His Thr Lys Arg Ala Ser Ala
1 5 10 15

Thr Val Lys Thr Ala Val Leu Ala Thr Leu Leu Phe Ala Thr Val Gln
20 25 30

Ala Asn Ala Thr
35

<210> 142
<211> 36
<212> PRT
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<220>
<223> Description of Artificial Sequence: homology

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<223> absent or positive

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<223> absent or positive

<400> 142
Val Xaa Val Ser Glu Leu Thr Arg Xaa His Thr Lys Arg Ala Ser Ala
1 5 10 15
Thr Val Xaa Thr Ala Val Leu Ala Thr Leu Leu Phe Ala Thr Val Gln
20 25 30
Ala Asn Ala Thr
35

<210> 143
<211> 36
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Hsf

<400> 143
Val Val Val Ser Glu Leu Thr Arg Thr His Thr Lys Arg Ala Ser Ala
1 5 10 15
Thr Val Glu Thr Ala Val Leu Ala Thr Leu Leu Phe Ala Thr Val Gln
20 25 30
Ala Asn Ala Thr
35

<210> 144
<211> 38

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Orf40a

<400> 144
Val Thr Leu Lys Ala Gly Asp Asn Leu Lys Ile Lys Gln Asn Thr Asn
1 5 10 15
Glu Asn Thr Asn Ala Ser Ser Phe Thr Tyr Ser Leu Lys Lys Asp Leu
20 25 30
Thr Gly Leu Ile Asn Val
35

<210> 145
<211> 38
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: homology

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<223> absent or positive

<220>
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<222> (36)..(37)
<223> absent or positive

<400> 145
Xaa Thr Leu Lys Ala Gly Asp Asn Leu Lys Ile Lys Gln Asn Thr Xaa
1 5 10 15
Glu Xaa Thr Asn Ala Ser Ser Phe Thr Tyr Ser Leu Lys Lys Asp Leu
20 25 30

Thr Xaa Leu Xaa Xaa Val
35

<210> 146
<211> 38
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Hsf

<400> 146
Ile Thr Leu Lys Ala Gly Asp Asn Leu Lys Ile Lys Gln Asn Thr Asp
1 5 10 15
Glu Ser Thr Asn Ala Ser Ser Phe Thr Tyr Ser Leu Lys Lys Asp Leu
20 25 30

Thr Asp Leu Thr Ser Val
35

<210> 147
<211> 29
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Orf40a

<400> 147
Val Thr Glu Lys Leu Ser Phe Gly Ala Asn Gly Lys Lys Val Asn Ile
1 5 10 15
Ile Ser Asp Thr Lys Gly Leu Asn Phe Ala Lys Glu Thr
20 25

<210> 148
<211> 29
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: homology

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<220>
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<222> (7)
<223> absent or positive

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<221> SITE
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<223> absent or positive

<220>
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<222> (28)..(29)
<223> absent or positive

<400> 148
Val Xaa Xaa Lys Leu Ser Xaa Gly Xaa Asn Gly Xaa Lys Val Asn Ile
1 5 10 15
Xaa Ser Asp Thr Lys Gly Leu Asn Phe Ala Lys Xaa Xaa
20 25

<210> 149
<211> 29
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Hsf

<400> 149
Val Ser Asp Lys Leu Ser Leu Gly Thr Asn Gly Asn Lys Val Asn Ile
1 5 10 15
Thr Ser Asp Thr Lys Gly Leu Asn Phe Ala Lys Asp Ser
20 25

<210> 150
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: ORF40a

<400> 150
Thr Asn Gly Asp Thr Thr Val His Leu Asn Gly Ile Gly Ser Thr Leu
1 5 10 15
Thr Asp Thr Leu Ala Gly Ser Ser Ala Ser His Val Asp Ala Gly Asn
20 25 30

<210> 151
<211> 32
<212> PRT
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<220>
<223> Description of Artificial Sequence: homology

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<400> 151
Thr Xaa Xaa Asp Xaa Xaa Xaa His Leu Asn Gly Ile Xaa Ser Thr Leu
1 5 10 15

Thr Asp Thr Leu Xaa Xaa Ser Xaa Ala Xaa Xaa Xaa Xaa Xaa Gly Asn
20 25 30

<210> 152
<211> 32
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Hsf

<400> 152

Thr Gly Asp Asp Ala Asn Ile His Leu Asn Gly Ile Ala Ser Thr Leu
1 5 10 15

Thr Asp Thr Leu Leu Asn Ser Gly Ala Thr Thr Asn Leu Gly Gly Asn
20 25 30

<210> 153

<211> 19

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: ORF40a

<400> 153

Arg Ala Ala Ser Ile Lys Asp Val Leu Asn Ala Gly Trp Asn Ile Lys
1 5 10 15

Gly Val Lys

<210> 154

<211> 19

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: homology

<220>

<221> SITE

<222> (5)

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<220>

<221> SITE

<222> (15)..(16)

<223> absent or positive

<400> 154

Arg Ala Ala Ser Xaa Lys Asp Val Leu Asn Ala Gly Trp Asn Xaa Xaa
1 5 10 15

Gly Val Lys

<210> 155

<211> 19

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Hsf

<400> 155

Arg Ala Ala Ser Val Lys Asp Val Leu Asn Ala Gly Trp Asn Val Arg
1 5 10 15

Gly Val Lys

<210> 156

<211> 28

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: ORF40a

<400> 156

Ser Thr Thr Gly Gln Ser Glu Asn Val Asp Phe Val Arg Thr Tyr Asp
1 5 10 15

Thr Val Glu Phe Leu Ser Ala Asp Thr Thr Thr Thr
20 25

<210> 157

<211> 28

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: homology

<220>

<221> SITE

<222> (2)..(4)

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<221> SITE

<222> (6)

<223> absent or positive

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<221> SITE

<222> (9)

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<221> SITE

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<223> absent or positive

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<221> SITE
<222> (23)
<223> absent or positive

<220>
<221> SITE
<222> (25)..(26)
<223> absent or positive

<400> 157
Ser Xaa Xaa Xaa Gln Xaa Glu Asn Xaa Asp Phe Val Xaa Thr Tyr Asp
1 5 10 15
Thr Val Xaa Phe Xaa Ser Xaa Asp Xaa Xaa Thr Thr
20 25

<210> 158
<211> 28
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Hsf

<400> 158
Ser Ala Asn Asn Gln Val Glu Asn Ile Asp Phe Val Ala Thr Tyr Asp
1 5 10 15
Thr Val Asp Phe Val Ser Gly Asp Lys Asp Thr Thr
20 25

<210> 159
<211> 240
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: ORF38a

<400> 159
Met Leu Arg Leu Thr Ala Leu Ala Val Cys Thr Ala Leu Ala Leu Gly
1 5 10 15
Ala Cys Ser Pro Gln Asn Ser Asp Ser Ala Pro Gln Ala Lys Glu Gln

20					25					30						
Ala	Val	Ser	Ala	Ala	Gln	Ser	Glu	Gly	Val	Ser	Val	Thr	Val	Lys	Thr	
35					40					45						
Ala	Arg	Gly	Asp	Val	Gln	Ile	Pro	Gln	Asn	Pro	Glu	Arg	Ile	Ala	Val	
50					55					60						
Tyr	Asp	Leu	Gly	Met	Leu	Asp	Thr	Leu	Ser	Lys	Leu	Gly	Val	Lys	Thr	
65					70					75					80	
Gly	Leu	Ser	Val	Asp	Lys	Asn	Arg	Leu	Pro	Tyr	Leu	Glu	Glu	Tyr	Phe	
85					90					95						
Lys	Thr	Thr	Lys	Pro	Ala	Gly	Thr	Leu	Phe	Glu	Pro	Asp	Tyr	Glu	Thr	
100					105					110						
Leu	Asn	Ala	Tyr	Lys	Pro	Gln	Leu	Ile	Ile	Ile	Gly	Ser	Arg	Ala	Ala	
115					120					125						
Lys	Ala	Phe	Asp	Lys	Leu	Asn	Glu	Ile	Ala	Pro	Thr	Ile	Glu	Met	Thr	
130					135					140						
Ala	Asp	Thr	Ala	Asn	Leu	Lys	Glu	Ser	Ala	Lys	Glu	Arg	Ile	Asp	Ala	
145					150					155					160	
Leu	Ala	Gln	Ile	Phe	Gly	Lys	Lys	Ala	Glu	Ala	Asp	Lys	Leu	Lys	Ala	
165					170					175						
Glu	Ile	Asp	Ala	Ser	Phe	Glu	Ala	Ala	Lys	Thr	Ala	Ala	Gln	Gly	Lys	
180					185					190						
Gly	Lys	Gly	Leu	Val	Ile	Leu	Val	Asn	Gly	Gly	Lys	Met	Ser	Ala	Phe	
195					200					205						
Gly	Pro	Ser	Ser	Arg	Leu	Gly	Gly	Trp	Leu	His	Lys	Asp	Ile	Gly	Val	
210					215					220						
Pro	Ala	Val	Asp	Glu	Ala	Ile	Lys	Glu	Gly	Ser	His	Gly	Gln	Pro	Ile	
225					230					235					240	

<210> 160

<211> 94

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: ORF38

<400> 160

Glu	Gly	Ala	Ser	Val	Thr	Val	Lys	Thr	Ala	Arg	Gly	Asp	Val	Gln	Ile
1				5					10					15	

Pro Gln Asn Pro Glu Arg Ile Ala Val Tyr Asp Leu Gly Met Leu Asp
 20 25 30
 Thr Leu Ser Lys Leu Gly Val Lys Thr Gly Leu Ser Val Asp Lys Asn
 35 40 45
 Arg Leu Pro Tyr Leu Glu Glu Tyr Phe Lys Thr Thr Lys Pro Ala Gly
 50 55 60
 Thr Leu Phe Glu Pro Asp Tyr Glu Thr Leu Asn Ala Tyr Lys Pro Gln
 65 70 75 80
 Leu Ile Ile Ile Gly Ser Arg Ala Ala Lys Ala Phe Asp Lys
 85 90

<210> 161
 <211> 96
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: overlap identity

<220>
 <221> SITE
 <222> (3)
 <223> absent or positive

<220>
 <221> SITE
 <222> (5)..(6)
 <223> absent or positive

<220>
 <221> SITE
 <222> (9)..(11)
 <223> absent or positive

<220>
 <221> SITE
 <222> (13)..(16)
 <223> absent or positive

<220>
 <221> SITE
 <222> (18)
 <223> absent or positive

<220>
 <221> SITE
 <222> (21)..(26)
 <223> absent or positive

<220>
 <221> SITE
 <222> (30)

<223> absent or positive

<220>

<221> SITE

<222> (34)..(36)

<223> absent or positive

<220>

<221> SITE

<222> (38)..(45)

<223> absent or positive

<220>

<221> SITE

<222> (47)..(50)

<223> absent or positive

<220>

<221> SITE

<222> (53)..(57)

<223> absent or positive

<220>

<221> SITE

<222> (60)..(64)

<223> absent or positive

<220>

<221> SITE

<222> (66)..(70)

<223> absent or positive

<220>

<221> SITE

<222> (72)

<223> absent or positive

<220>

<221> SITE

<222> (74)..(75)

<223> absent or positive

<220>

<221> SITE

<222> (78)

<223> absent or positive

<220>

<221> SITE

<222> (81)

<223> absent or positive

<220>

<221> SITE

<222> (86)..(87)

<223> absent or positive

<220>
 <221> SITE
 <222> (89)..(90)
 <223> absent or positive

<220>
 <221> SITE
 <222> (92)..(93)
 <223> absent or positive

<400> 161
 Glu Gly Xaa Ser Xaa Xaa Val Lys Xaa Xaa Xaa Gly Xaa Xaa Xaa Xaa
 1 5 10 15
 Pro Xaa Asn Pro Xaa Xaa Xaa Xaa Xaa Xaa Asp Leu Gly Xaa Leu Asp
 20 25 30
 Thr Xaa Xaa Xaa Leu Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Val Xaa Xaa
 35 40 45
 Xaa Xaa Leu Pro Xaa Xaa Xaa Xaa Xaa Phe Lys Xaa Xaa Xaa Xaa Xaa
 50 55 60
 Gly Xaa Xaa Xaa Xaa Xaa Asp Xaa Glu Xaa Xaa Asn Ala Xaa Lys Pro
 65 70 75 80
 Xaa Leu Ile Ile Ile Xaa Xaa Arg Xaa Xaa Lys Xaa Xaa Asp Lys Leu
 85 90 95

<210> 162
 <211> 96
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Lipo

<400> 162
 Glu Gly Asp Ser Phe Leu Val Lys Asp Ser Leu Gly Glu Asn Lys Thr
 1 5 10 15
 Pro Lys Asn Pro Ser Lys Val Val Ile Leu Asp Leu Gly Ile Leu Asp
 20 25 30
 Thr Phe Asp Ala Leu Lys Leu Asn Asp Lys Val Ala Gly Val Pro Ala
 35 40 45
 Lys Asn Leu Pro Lys Tyr Leu Gln Gln Phe Lys Asn Lys Pro Ser Val
 50 55 60
 Gly Gly Val Gln Gln Val Asp Phe Glu Ala Ile Asn Ala Leu Lys Pro
 65 70 75 80
 Asp Leu Ile Ile Ile Ser Gly Arg Gln Ser Lys Phe Tyr Asp Lys Leu
 85 90 95

<210> 163
<211> 91
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: ORF44

<400> 163
Thr Val Ser Tyr Val Cys Gln Gln Gly Lys Lys Val Lys Val Thr Tyr
1 5 10 15
Gly Phe Asn Lys Gln Gly Leu Thr Thr Tyr Ala Ser Ala Val Ile Asn
20 25 30
Gly Lys Arg Val Gln Met Pro Val Asn Leu Asp Lys Ser Asp Asn Val
35 40 45
Glu Thr Phe Tyr Gly Lys Glu Gly Gly Tyr Val Leu Gly Thr Gly Val
50 55 60
Met Asp Gly Lys Ser Tyr Arg Lys Gln Pro Ile Met Ile Thr Ala Pro
65 70 75 80
Asp Asn Gln Ile Val Phe Lys Asp Cys Ser Pro
85 90

<210> 164
<211> 91
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: overlap identity

<220>
<221> SITE
<222> (1)
<223> absent or positive

<220>
<221> SITE
<222> (3)
<223> absent or positive

<220>
<221> SITE
<222> (10)..(13)
<223> absent or positive

<220>
<221> SITE

<222> (15)
<223> absent or positive

<220>
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<222> (17)
<223> absent or positive

<220>
<221> SITE
<222> (20)..(21)
<223> absent or positive

<220>
<221> SITE
<222> (23)..(24)
<223> absent or positive

<220>
<221> SITE
<222> (26)
<223> absent or positive

<220>
<221> SITE
<222> (28)..(31)
<223> absent or positive

<220>
<221> SITE
<222> (33)..(38)
<223> absent or positive

<220>
<221> SITE
<222> (40)
<223> absent or positive

<220>
<221> SITE
<222> (43)..(44)
<223> absent or positive

<220>
<221> SITE
<222> (49)
<223> absent or positive

<220>
<221> SITE
<222> (51)..(56)
<223> absent or positive

<220>
<221> SITE
<222> (59)
<223> absent or positive

<220>
 <221> SITE
 <222> (61)
 <223> absent or positive

<220>
 <221> SITE
 <222> (63)..(64)
 <223> absent or positive

<220>
 <221> SITE
 <222> (67)..(69)
 <223> absent or positive

<220>
 <221> SITE
 <222> (72)
 <223> absent or positive

<220>
 <221> SITE
 <222> (74)
 <223> absent or positive

<220>
 <221> SITE
 <222> (76)..(78)
 <223> absent or positive

<220>
 <221> SITE
 <222> (81)..(82)
 <223> absent or positive

<220>
 <221> SITE
 <222> (84)..(86)
 <223> absent or positive

<400> 164
 Xaa Val Xaa Tyr Val Cys Gln Gln Gly Xaa Xaa Xaa Xaa Val Xaa Tyr
 1 5 10 15
 Xaa Phe Asn Xaa Xaa Gly Xaa Xaa Thr Xaa Ala Xaa Xaa Xaa Xaa Asn
 20 25 30
 Xaa Xaa Xaa Xaa Xaa Xaa Pro Xaa Asn Leu Xaa Xaa Ser Asp Asn Val
 35 40 45
 Xaa Thr Xaa Xaa Xaa Xaa Xaa Xaa Gly Tyr Xaa Leu Xaa Thr Xaa Xaa
 50 55 60
 Met Asp Xaa Xaa Xaa Tyr Arg Xaa Gln Xaa Ile Xaa Xaa Xaa Ala Pro
 65 70 75 80

Xaa Xaa Gln Xaa Xaa Xaa Lys Asp Cys Ser Pro
85 90

<210> 165
<211> 90
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: LecA

<400> 165
Ser Val Ala Tyr Val Cys Gln Gln Gly Arg Arg Leu Asn Val Asn Tyr
1 5 10 15
Arg Phe Asn Ser Ala Gly Val Pro Thr Ser Ala Glu Leu Arg Val Asn
20 25 30
Asn Arg Asn Leu Arg Leu Pro Tyr Asn Leu Ser Ala Ser Asp Asn Val
35 40 45
Asp Thr Val Phe Ser Ala Asn Gly Tyr Arg Leu Thr Thr Asn Ala Met
50 55 60
Asp Ser Ala Asn Tyr Arg Ser Gln Asp Ile Ile Val Ser Ala Pro Asn
65 70 75 80
Gly Gln Met Leu Tyr Lys Asp Cys Ser Pro
85 90

<210> 166
<211> 240
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: ORF49a

<220>
<221> SITE
<222> (18)
<223> place-holder

<220>
<221> SITE
<222> (48)
<223> place-holder

<220>
<221> SITE
<222> (195)
<223> place-holder

<400> 166
Ser Lys Asn Glu Leu Asn Glu Thr Lys Leu Pro Val Arg Val Val Ala

1	5	10	15
Gln Xaa Ala Ala Thr Arg Ser Gly Trp Asp Thr Val Leu Glu Gly Thr	20	25	30
Glu Phe Lys Thr Thr Leu Ala Gly Ala Asp Ile Gln Ala Gly Val Xaa	35	40	45
Glu Lys Ala Arg Val Asp Ala Lys Ile Ile Leu Lys Gly Ile Val Asn	50	55	60
Arg Ile Gln Ser Glu Glu Lys Leu Glu Thr Asn Ser Thr Val Trp Gln	65	70	75
Lys Gln Ala Gly Arg Gly Ser Thr Ile Glu Thr Leu Lys Leu Pro Ser	85	90	95
Phe Glu Ser Pro Thr Pro Pro Lys Leu Ser Ala Pro Gly Gly Tyr Ile	100	105	110
Val Asp Ile Pro Lys Gly Asn Leu Lys Thr Glu Ile Glu Lys Leu Ser	115	120	125
Lys Gln Pro Glu Tyr Ala Tyr Leu Lys Gln Leu Gln Val Ala Lys Asn	130	135	140
Ile Asn Trp Asn Gln Val Gln Leu Ala Tyr Asp Arg Trp Asp Tyr Lys	145	150	155
Gln Glu Gly Leu Thr Glu Ala Gly Ala Ala Ile Ile Ala Leu Ala Val	165	170	175
Thr Val Val Thr Ser Gly Ala Gly Thr Gly Ala Val Leu Gly Leu Asn	180	185	190
Gly Ala Xaa Ala Ala Ala Thr Asp Ala Ala Phe Ala Ser Leu Ala Ser	195	200	205
Gln Ala Ser Val Ser Phe Ile Asn Asn Lys Gly Asp Val Gly Lys Thr	210	215	220
Leu Lys Glu Leu Gly Arg Ser Ser Thr Val Lys Asn Leu Val Val Ala	225	230	235
			240

<210> 167
 <211> 540
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: ORF49a

<220>
 <221> SITE
 <222> (1)

<223> place-holder

<220>

<221> SITE

<222> (29)

<223> place-holder

<220>

<221> SITE

<222> (50)

<223> place-holder

<220>

<221> SITE

<222> (80)

<223> place-holder

<220>

<221> SITE

<222> (227)

<223> place-holder

<220>

<221> SITE

<222> (288)

<223> place-holder

<220>

<221> SITE

<222> (324)

<223> place-holder

<220>

<221> SITE

<222> (446)

<223> place-holder

<220>

<221> SITE

<222> (463)

<223> place-holder

<400> 167

Xaa	Gln	Leu	Leu	Ala	Glu	Glu	Gly	Ile	His	Lys	His	Glu	Leu	Asp	Val
1				5					10					15	

Gln	Lys	Ser	Arg	Arg	Phe	Ile	Gly	Ile	Lys	Val	Gly	Xaa	Ser	Asn	Tyr
			20					25						30	

Ser	Lys	Asn	Glu	Leu	Asn	Glu	Thr	Lys	Leu	Pro	Val	Arg	Val	Val	Ala
		35					40					45			

Gln	Xaa	Ala	Ala	Thr	Arg	Ser	Gly	Trp	Asp	Thr	Val	Leu	Glu	Gly	Thr
	50					55					60				

Glu	Phe	Lys	Thr	Thr	Leu	Ala	Gly	Ala	Asp	Ile	Gln	Ala	Gly	Val	Xaa
65					70					75					80

Glu Lys Ala Arg Val Asp Ala Lys Ile Ile Leu Lys Gly Ile Val Asn
 85 90 95

Arg Ile Gln Ser Glu Glu Lys Leu Glu Thr Asn Ser Thr Val Trp Gln
 100 105 110

Lys Gln Ala Gly Arg Gly Ser Thr Ile Glu Thr Leu Lys Leu Pro Ser
 115 120 125

Phe Glu Ser Pro Thr Pro Pro Lys Leu Ser Ala Pro Gly Gly Tyr Ile
 130 135 140

Val Asp Ile Pro Lys Gly Asn Leu Lys Thr Glu Ile Glu Lys Leu Ser
 145 150 155 160

Lys Gln Pro Glu Tyr Ala Tyr Leu Lys Gln Leu Gln Val Ala Lys Asn
 165 170 175

Ile Asn Trp Asn Gln Val Gln Leu Ala Tyr Asp Arg Trp Asp Tyr Lys
 180 185 190

Gln Glu Gly Leu Thr Glu Ala Gly Ala Ala Ile Ile Ala Leu Ala Val
 195 200 205

Thr Val Val Thr Ser Gly Ala Gly Thr Gly Ala Val Leu Gly Leu Asn
 210 215 220

Gly Ala Xaa Ala Ala Ala Thr Asp Ala Ala Phe Ala Ser Leu Ala Ser
 225 230 235 240

Gln Ala Ser Val Ser Phe Ile Asn Asn Lys Gly Asp Val Gly Lys Thr
 245 250 255

Leu Lys Glu Leu Gly Arg Ser Ser Thr Val Lys Asn Leu Val Val Ala
 260 265 270

Ala Ala Thr Ala Gly Val Ala Asp Lys Ile Gly Ala Ser Ala Leu Xaa
 275 280 285

Asn Val Ser Asp Lys Gln Trp Ile Asn Asn Leu Thr Val Asn Leu Ala
 290 295 300

Asn Ala Gly Ser Ala Ala Leu Ile Asn Thr Ala Val Asn Gly Gly Ser
 305 310 315 320

Leu Lys Asp Xaa Leu Glu Ala Asn Ile Leu Ala Ala Leu Val Asn Thr
 325 330 335

Ala His Gly Glu Ala Ala Ser Lys Ile Lys Gln Leu Asp Gln His Tyr
 340 345 350

Ile Val His Lys Ile Ala His Ala Ile Ala Gly Cys Ala Ala Ala Ala
 355 360 365

Ala Asn Lys Gly Lys Cys Gln Asp Gly Ala Ile Gly Ala Ala Val Gly
 370 375 380

Glu Ile Val Gly Glu Ala Leu Thr Asn Gly Lys Asn Pro Asp Thr Leu

385		390		395		400									
Thr	Ala	Lys	Glu	Arg	Glu	Gln	Ile	Leu	Ala	Tyr	Ser	Lys	Leu	Val	Ala
				405					410					415	
Gly	Thr	Val	Ser	Gly	Val	Val	Gly	Gly	Asp	Val	Asn	Ala	Ala	Ala	Asn
			420					425						430	
Ala	Ala	Glu	Val	Ala	Val	Lys	Asn	Asn	Gln	Leu	Ser	Asp	Xaa	Glu	Gly
		435					440					445			
Arg	Glu	Phe	Asp	Asn	Glu	Met	Thr	Ala	Cys	Ala	Lys	Gln	Asn	Xaa	Pro
	450					455					460				
Gln	Leu	Cys	Arg	Lys	Asn	Thr	Val	Lys	Lys	Tyr	Gln	Asn	Val	Ala	Asp
465					470					475					480
Lys	Arg	Leu	Ala	Ala	Ser	Ile	Ala	Ile	Cys	Thr	Asp	Ile	Ser	Arg	Ser
				485					490					495	
Thr	Glu	Cys	Arg	Thr	Ile	Arg	Lys	Gln	His	Leu	Ile	Asp	Ser	Arg	Ser
			500					505					510		
Leu	His	Ser	Ser	Trp	Glu	Ala	Gly	Leu	Ile	Gly	Lys	Asp	Asp	Glu	Trp
	515						520					525			
Tyr	Lys	Leu	Phe	Ser	Lys	Ser	Tyr	Thr	Gln	Ala	Asp				
	530					535					540				

<210> 168
 <211> 540
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: ORF49-1

<400> 168
Met Gln Leu Leu Ala Ala Glu Gly Ile His Gln His Gln Leu Asn Val
1 5 10 15
Gln Lys Ser Thr Arg Phe Ile Gly Ile Lys Val Gly Lys Ser Asn Tyr
20 25 30
Ser Lys Asn Glu Leu Asn Glu Thr Lys Leu Pro Val Arg Val Ile Ala
35 40 45
Gln Thr Ala Lys Thr Arg Ser Gly Trp Asp Thr Val Leu Glu Gly Thr
50 55 60
Glu Phe Lys Thr Thr Leu Ser Gly Ala Asp Ile Gln Ala Gly Val Gly
65 70 75 80
Glu Lys Ala Arg Ala Asp Ala Lys Ile Ile Leu Lys Gly Ile Val Asn
85 90 95

Arg Ile Gln Thr Glu Glu Lys Leu Glu Ser Asn Ser Thr Val Trp Gln
 100 105 110
 Lys Gln Ala Gly Ser Gly Ser Thr Val Glu Thr Leu Lys Leu Pro Ser
 115 120 125
 Phe Glu Gly Pro Ala Leu Pro Lys Leu Thr Ala Pro Gly Gly Tyr Ile
 130 135 140
 Ala Asp Ile Pro Lys Gly Asn Leu Lys Thr Glu Ile Glu Lys Leu Ala
 145 150 155 160
 Lys Gln Pro Glu Tyr Ala Tyr Leu Lys Gln Leu Gln Thr Val Lys Asp
 165 170 175
 Val Asn Trp Asn Gln Val Gln Leu Ala Tyr Asp Lys Trp Asp Tyr Lys
 180 185 190
 Gln Glu Gly Leu Thr Gly Ala Gly Ala Ala Ile Ile Ala Leu Ala Val
 195 200 205
 Thr Val Val Thr Ser Gly Ala Gly Thr Gly Ala Val Leu Gly Leu Asn
 210 215 220
 Gly Ala Ala Ala Ala Ala Thr Asp Ala Ala Phe Ala Ser Leu Ala Ser
 225 230 235 240
 Gln Ala Ser Val Ser Phe Ile Asn Asn Lys Gly Asn Ile Gly Asn Thr
 245 250 255
 Leu Lys Glu Leu Gly Arg Ser Ser Thr Val Lys Asn Leu Met Val Ala
 260 265 270
 Val Ala Thr Ala Gly Val Ala Asp Lys Ile Gly Ala Ser Ala Leu Asn
 275 280 285
 Asn Val Ser Asp Lys Gln Trp Ile Asn Asn Leu Thr Val Asn Leu Ala
 290 295 300
 Asn Ala Gly Ser Ala Ala Leu Ile Asn Thr Ala Val Asn Gly Gly Ser
 305 310 315 320
 Leu Lys Asp Asn Leu Glu Ala Asn Ile Leu Ala Ala Leu Val Asn Thr
 325 330 335
 Ala His Gly Glu Ala Ala Ser Lys Ile Lys Gln Leu Asp Gln His Tyr
 340 345 350
 Ile Ala His Lys Ile Ala His Ala Ile Ala Gly Cys Ala Ala Ala Ala
 355 360 365
 Ala Asn Lys Gly Lys Cys Gln Asp Gly Ala Ile Gly Ala Ala Val Gly
 370 375 380
 Glu Ile Leu Gly Glu Thr Leu Leu Asp Gly Arg Asp Pro Gly Ser Leu
 385 390 395 400

Asn Val Lys Asp Arg Ala Lys Ile Ile Ala Lys Ala Lys Leu Ala Ala
 405 410 415
 Gly Ala Val Ala Ala Leu Ser Lys Gly Asp Val Ser Thr Ala Ala Asn
 420 425 430
 Ala Ala Ala Val Ala Val Glu Asn Asn Ser Leu Asn Asp Ile Gln Asp
 435 440 445
 Arg Leu Leu Ser Gly Asn Tyr Ala Leu Cys Met Ser Ala Gly Gly Ala
 450 455 460
 Glu Ser Phe Cys Glu Ser Tyr Arg Pro Leu Gly Leu Pro His Phe Val
 465 470 475 480
 Ser Val Ser Gly Glu Met Lys Leu Pro Asn Lys Phe Gly Asn Arg Met
 485 490 495
 Val Asn Gly Lys Leu Ile Ile Asn Thr Arg Asn Gly Asn Val Tyr Phe
 500 505 510
 Ser Val Gly Lys Ile Trp Ser Thr Val Lys Ser Thr Lys Ser Asn Ile
 515 520 525
 Ser Gly Val Ser Val Gly Trp Val Leu Asn Val Ser
 530 535 540

<210> 169
 <211> 210
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: ORF39

<220>
 <221> SITE
 <222> (166)..(193)
 <223> place-holder

<400> 169
 Lys Phe Asp Phe Thr Trp Phe Ile Pro Ala Val Ile Lys Tyr Arg Arg
 1 5 10 15
 Leu Phe Phe Glu Val Leu Val Val Ser Val Val Leu Gln Leu Phe Ala
 20 25 30
 Leu Ile Thr Pro Leu Phe Phe Gln Val Val Met Asp Lys Val Leu Val
 35 40 45
 His Arg Gly Phe Ser Thr Leu Asp Val Val Ser Val Ala Leu Leu Val
 50 55 60
 Val Ser Leu Phe Glu Ile Val Leu Gly Gly Leu Arg Thr Tyr Leu Phe
 65 70 75 80

Ala His Thr Thr Ser Arg Ile Asp Val Glu Leu Gly Ala Arg Leu Phe
 85 90 95
 Arg His Leu Leu Ser Leu Pro Leu Ser Tyr Phe Glu His Arg Arg Val
 100 105 110

 Gly Asp Thr Val Ala Arg Val Arg Glu Leu Glu Gln Ile Arg Asn Phe
 115 120 125

 Leu Thr Gly Gln Ala Leu Thr Ser Val Leu Asp Leu Ala Phe Ser Phe
 130 135 140

 Ile Phe Leu Ala Val Met Trp Tyr Tyr Ser Ser Thr Leu Thr Trp Val
 145 150 155 160

 Val Leu Ala Ser Leu Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 165 170 175

 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 180 185 190

 Xaa Ile Cys Ala Asn Arg Thr Val Leu Ile Ile Ala His Arg Leu Ser
 195 200 205

 Thr Val
 210

<210> 170
 <211> 240
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: ORF39a

<400> 170
 Ala Val Leu Ser Phe Ala Glu Phe Ser Asn Arg Tyr Ser Gly Lys Leu
 1 5 10 15

 Ile Leu Val Ala Ser Arg Ala Ser Val Leu Gly Ser Leu Ala Lys Phe
 20 25 30

 Asp Phe Thr Trp Phe Ile Pro Ala Val Ile Lys Tyr Arg Arg Leu Phe
 35 40 45

 Phe Glu Val Leu Val Val Ser Val Val Leu Gln Leu Phe Ala Leu Ile
 50 55 60

 Thr Pro Leu Phe Phe Gln Val Val Met Asp Lys Val Leu Val His Arg
 65 70 75 80

 Gly Phe Ser Thr Leu Asp Val Val Ser Val Ala Leu Leu Val Val Ser
 85 90 95

 Leu Phe Glu Ile Val Leu Gly Gly Leu Arg Thr Tyr Leu Phe Ala His
 100 105 110

Thr Thr Ser Arg Ile Asp Val Glu Leu Gly Ala Arg Leu Phe Arg His
 115 120 125
 Leu Leu Ser Leu Pro Leu Ser Tyr Phe Glu His Arg Arg Val Gly Asp
 130 135 140
 Thr Val Ala Arg Val Arg Glu Leu Glu Gln Ile Arg Asn Phe Leu Thr
 145 150 155 160
 Gly Gln Ala Leu Thr Ser Val Leu Asp Leu Ala Phe Ser Phe Ile Phe
 165 170 175
 Leu Ala Val Met Trp Tyr Tyr Ser Ser Thr Leu Thr Trp Val Val Leu
 180 185 190
 Ala Ser Leu Pro Ala Tyr Ala Phe Trp Ser Ala Phe Ile Ser Pro Ile
 195 200 205
 Leu Arg Thr Arg Leu Asn Asp Lys Phe Ala Arg Asn Ala Asp Asn Gln
 210 215 220
 Ser Phe Leu Val Glu Ser Ile Thr Ala Val Gly Thr Val Lys Ala Met
 225 230 235 240

<210> 171
 <211> 690
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: ORF39a

<220>
 <221> SITE
 <222> (29)..(40)
 <223> place-holder

<220>
 <221> SITE
 <222> (137)..(153)
 <223> place-holder

<220>
 <221> SITE
 <222> (173)..(187)
 <223> place-holder

<400> 171
 Tyr His Gly Ile Ala Ala Asn Pro Ala Asp Ile Gln His Glu Phe Cys
 1 5 10 15

Thr Ser Ala Gln Ser Asp Leu Asn Glu Thr Gln Trp Xaa Xaa Xaa Xaa
 20 25 30

Thr Gln Arg Trp Asp Asn Gln Leu Ala Ala Tyr Val Ala Ser Gly Phe
 340 345 350
 Arg Val Thr Lys Leu Ala Val Val Gly Gln Gln Gly Val Gln Leu Ile
 355 360 365
 Gln Lys Leu Val Thr Val Ala Thr Leu Trp Ile Gly Ala Arg Leu Val
 370 375 380
 Ile Glu Ser Lys Leu Thr Val Gly Gln Leu Ile Ala Phe Asn Met Leu
 385 390 395 400
 Ser Gly Gln Val Ala Ala Pro Val Ile Arg Leu Ala Gln Leu Trp Gln
 405 410 415
 Asp Phe Gln Gln Val Gly Ile Ser Val Ala Arg Leu Gly Asp Ile Leu
 420 425 430
 Asn Ala Pro Thr Glu Asn Ala Ser Ser His Leu Ala Leu Pro Asp Ile
 435 440 445
 Arg Gly Glu Ile Thr Phe Glu His Val Asp Phe Arg Tyr Lys Ala Asp
 450 455 460
 Gly Arg Leu Ile Leu Gln Asp Leu Asn Leu Arg Ile Arg Ala Gly Glu
 465 470 475 480
 Val Leu Gly Ile Val Gly Arg Ser Gly Ser Gly Lys Ser Thr Leu Thr
 485 490 495
 Lys Leu Val Gln Arg Leu Tyr Val Pro Ala Gln Gly Arg Val Leu Val
 500 505 510
 Asp Gly Asn Asp Leu Ala Leu Ala Ala Pro Ala Trp Leu Arg Arg Gln
 515 520 525
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 Glu Ala Ala Lys Leu Ala Gly Ala His Glu Phe Ile Met Glu Leu Pro
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 Glu Gly Tyr Gly Thr Val Val Gly Glu Gln Gly Ala Gly Leu Ser Gly
 580 585 590
 Gly Gln Arg Gln Arg Ile Ala Ile Ala Arg Ala Leu Ile Thr Asn Pro
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 Arg Ile Leu Ile Phe Asp Glu Ala Thr Ser Ala Leu Asp Tyr Glu Ser
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 Glu Arg Ala Ile Met Gln Asn Met Gln Ala Ile Cys Ala Asn Arg Thr
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 Val Leu Ile Ile Ala His Arg Leu Ser Thr Val Lys Thr Ala His Arg

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Ile Ile Ala Met Asp Lys Gly Arg Ile Val Glu Ala Gly Thr Gln Gln					
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 20 25 30
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Val Xaa Xaa Xaa Ile Xaa Arg
 35 40 45
 Leu Ala Xaa Xaa Xaa Leu Pro Ala Leu Val Trp Xaa Xaa Asp Gly Xaa
 50 55 60
 His Phe Ile Leu Xaa Lys Xaa Asp Xaa Xaa Xaa Glu Xaa Xaa Xaa Tyr
 65 70 75 80
 Leu Ile Xaa Asp Leu Xaa Thr Xaa Xaa Xaa Xaa Xaa Leu Xaa Xaa Ala
 85 90 95
 Glu Phe Xaa Xaa Xaa Tyr Xaa Gly Lys Leu Ile Leu Val Ala Ser Arg
 100 105 110

Ala Ser Xaa Xaa Gly Xaa Leu Ala Lys Phe Asp Phe Thr Trp Phe Ile
 115 120 125
 Pro Ala Val Ile Lys Tyr Arg Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
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 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Ile Thr Pro Leu Phe Phe Gln
 145 150 155 160
 Val Val Met Asp Lys Val Leu Val His Arg Gly Phe Xaa Xaa Xaa Xaa
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 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Phe Glu Ile Val Leu
 180 185 190
 Xaa Gly Leu Arg Thr Tyr Xaa Phe Ala His Xaa Thr Ser Arg Ile Asp
 195 200 205
 Val Glu Leu Gly Ala Arg Leu Phe Arg His Leu Leu Xaa Leu Pro Xaa
 210 215 220
 Ser Tyr Phe Glu Xaa Arg Arg Val Gly Asp Thr Val Ala Arg Val Arg
 225 230 235 240
 Glu Leu Xaa Gln Ile Arg Asn Phe Leu Thr Gly Gln Ala Leu Thr Ser
 245 250 255
 Val Leu Asp Leu Xaa Phe Ser Phe Ile Phe Xaa Ala Val Met Trp Tyr
 260 265 270
 Tyr Ser Xaa Xaa Leu Thr Xaa Val Xaa Leu Xaa Ser Leu Pro Xaa Tyr
 275 280 285
 Xaa Xaa Trp Ser Xaa Phe Ile Ser Pro Ile Leu Arg Xaa Arg Leu Xaa
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 Xaa Lys Phe Ala Arg Xaa Ala Asp Asn Gln Ser Phe Leu Val Glu Ser
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 Xaa Thr Ala Xaa Xaa Thr Xaa Lys Ala Xaa Ala Val Xaa Pro Gln Met
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 Arg Val Thr Xaa Leu Ala Xaa Xaa Gly Gln Gln Gly Val Gln Xaa Ile
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 Gln Lys Xaa Val Xaa Val Xaa Thr Leu Trp Xaa Gly Ala Xaa Leu Val
 370 375 380
 Ile Xaa Xaa Xaa Leu Xaa Xaa Gly Gln Leu Ile Ala Phe Asn Met Leu
 385 390 395 400
 Ser Gly Gln Val Xaa Ala Pro Val Ile Arg Leu Ala Gln Leu Trp Gln
 405 410 415
 Asp Phe Gln Gln Val Gly Ile Ser Val Xaa Arg Leu Gly Asp Xaa Leu

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Asn	Xaa	Pro	Thr	Glu	Xaa	Xaa	Xaa	Xaa	Xaa	Leu	Ala	Leu	Pro	Xaa	Ile
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Xaa	Gly	Xaa	Ile	Thr	Phe	Xaa	Xaa	Xaa	Xaa	Phe	Arg	Tyr	Lys	Xaa	Asp
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Val	Xaa	Gly	Ile	Val	Gly	Arg	Ser	Gly	Ser	Gly	Lys	Ser	Thr	Leu	Thr
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Lys	Leu	Xaa	Gln	Arg	Xaa	Tyr	Xaa	Pro	Xaa	Xaa	Gly	Xaa	Val	Leu	Xaa
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Asp	Gly	Xaa	Asp	Leu	Ala	Leu	Ala	Xaa	Pro	Xaa	Trp	Leu	Arg	Arg	Gln
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Val	Gly	Val	Val	Leu	Gln	Xaa	Asn	Val	Leu	Leu	Asn	Arg	Ser	Ile	Arg
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Asp	Asn	Ile	Ala	Leu	Xaa	Asp	Xaa	Gly	Met	Pro	Xaa	Glu	Xaa	Ile	Xaa
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Xaa	Ala	Ala	Lys	Leu	Ala	Gly	Ala	His	Glu	Phe	Ile	Xaa	Glu	Leu	Xaa
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Glu	Gly	Tyr	Xaa	Thr	Xaa	Val	Gly	Glu	Gln	Gly	Ala	Gly	Leu	Ser	Gly
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Gly	Gln	Arg	Gln	Arg	Ile	Ala	Ile	Ala	Arg	Ala	Leu	Xaa	Xaa	Asn	Pro
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Val	Xaa	Ile	Ile	Ala	His	Arg	Leu	Ser	Thr	Val	Lys	Xaa	Ala	Xaa	Arg
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Ile	Ile	Xaa	Met	Xaa	Lys	Gly	Xaa	Ile	Val	Glu	Xaa	Gly	Xaa	Xaa	Xaa
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Glu	Leu	Leu	Ala	Xaa	Pro	Asn	Gly	Xaa	Tyr	Xaa	Tyr	Leu	Xaa	Xaa	Leu
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Gln	Xaa														
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A. pleuropneumoniae

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Ser	Leu	Glu	Leu	Lys	Ala	Lys	Gln	Val	Lys	Lys	Ala	Ile	Asp	Arg	Leu
		35					40					45			
Ala	Phe	Ile	Ala	Leu	Pro	Ala	Leu	Val	Trp	Arg	Glu	Asp	Gly	Lys	His
	50					55					60				
Phe	Ile	Leu	Thr	Lys	Ile	Asp	Asn	Glu	Ala	Lys	Lys	Tyr	Leu	Ile	Phe
65					70					75					80
Asp	Leu	Glu	Thr	His	Asn	Pro	Arg	Ile	Leu	Glu	Gln	Ala	Glu	Phe	Glu
				85					90					95	
Ser	Leu	Tyr	Gln	Gly	Lys	Leu	Ile	Leu	Val	Ala	Ser	Arg	Ala	Ser	Ile
			100					105					110		
Val	Gly	Lys	Leu	Ala	Lys	Phe	Asp	Phe	Thr	Trp	Phe	Ile	Pro	Ala	Val
		115					120					125			
Ile	Lys	Tyr	Arg	Lys	Ile	Phe	Ile	Glu	Thr	Leu	Ile	Val	Ser	Ile	Phe
	130					135						140			
Leu	Gln	Ile	Phe	Ala	Leu	Ile	Thr	Pro	Leu	Phe	Phe	Gln	Val	Val	Met
145					150					155					160
Asp	Lys	Val	Leu	Val	His	Arg	Gly	Phe	Ser	Thr	Leu	Asn	Val	Ile	Thr
				165					170					175	
Val	Ala	Leu	Ala	Ile	Val	Val	Leu	Phe	Glu	Ile	Val	Leu	Asn	Gly	Leu
			180					185					190		
Arg	Thr	Tyr	Ile	Phe	Ala	His	Ser	Thr	Ser	Arg	Ile	Asp	Val	Glu	Leu
		195					200					205			
Gly	Ala	Arg	Leu	Phe	Arg	His	Leu	Leu	Ala	Leu	Pro	Ile	Ser	Tyr	Phe
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Glu	Asn	Arg	Arg	Val	Gly	Asp	Thr	Val	Ala	Arg	Val	Arg	Glu	Leu	Asp
225					230					235					240
Gln	Ile	Arg	Asn	Phe	Leu	Thr	Gly	Gln	Ala	Leu	Thr	Ser	Val	Leu	Asp
				245					250					255	
Leu	Met	Phe	Ser	Phe	Ile	Phe	Phe	Ala	Val	Met	Trp	Tyr	Tyr	Ser	Pro
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 325 330 335
 Trp Asp Lys Gln Leu Ala Ser Tyr Val Ser Ala Gly Phe Arg Val Thr
 340 345 350
 Thr Leu Ala Thr Ile Gly Gln Gln Gly Val Gln Phe Ile Gln Lys Val
 355 360 365
 Val Met Val Ile Thr Leu Trp Leu Gly Ala His Leu Val Ile Ser Gly
 370 375 380
 Asp Leu Ser Ile Gly Gln Leu Ile Ala Phe Asn Met Leu Ser Gly Gln
 385 390 395 400
 Val Ile Ala Pro Val Ile Arg Leu Ala Gln Leu Trp Gln Asp Phe Gln
 405 410 415
 Gln Val Gly Ile Ser Val Thr Arg Leu Gly Asp Val Leu Asn Ser Pro
 420 425 430
 Thr Glu Ser Tyr Gln Gly Lys Leu Ala Leu Pro Glu Ile Lys Gly Asp
 435 440 445
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 465 470 475 480
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 485 490 495
 Gln Arg Phe Tyr Ile Pro Glu Asn Gly Gln Val Leu Ile Asp Gly His
 500 505 510
 Asp Leu Ala Leu Ala Asp Pro Asn Trp Leu Arg Arg Gln Val Gly Val
 515 520 525
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 530 535 540
 Ala Leu Ala Asp Pro Gly Met Pro Met Glu Lys Ile Val His Ala Ala
 545 550 555 560
 Lys Leu Ala Gly Ala His Glu Phe Ile Ser Glu Leu Arg Glu Gly Tyr
 565 570 575
 Asn Thr Ile Val Gly Glu Gln Gly Ala Gly Leu Ser Gly Gly Gln Arg

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Gln	Arg	Ile	Ala	Ile	Ala	Arg	Ala	Leu	Val	Asn	Asn	Pro	Lys	Ile	Leu	
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Ile	Met	Arg	Asn	Met	His	Gln	Ile	Cys	Lys	Gly	Arg	Thr	Val	Ile	Ile	
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Ile	Ala	His	Arg	Leu	Ser	Thr	Val	Lys	Asn	Ala	Asp	Arg	Ile	Ile	Val	
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Met	Glu	Lys	Gly	Gln	Ile	Val	Glu	Gln	Gly	Lys	His	Lys	Glu	Leu	Leu	
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			20					25						30		
Xaa	Ile	Thr	Pro	Leu	Phe	Phe	Gln	Val	Val	Met	Asp	Lys	Val	Leu	Val	
		35					40					45				
His	Arg	Gly	Phe	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
		50				55						60				

Xaa	Xaa	Xaa	Phe	Glu	Ile	Val	Leu	Gly	Gly	Leu	Arg	Thr	Tyr	Leu	Phe
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Ala	His	Thr	Thr	Ser	Arg	Ile	Asp	Val	Glu	Leu	Gly	Ala	Arg	Leu	Phe
				85					90					95	
Arg	His	Leu	Leu	Ser	Leu	Pro	Leu	Ser	Tyr	Phe	Glu	His	Arg	Arg	Val
		100						105					110		
Gly	Asp	Thr	Val	Ala	Arg	Val	Arg	Glu	Leu	Glu	Gln	Ile	Arg	Asn	Phe
	115						120					125			
Leu	Thr	Gly	Gln	Ala	Leu	Thr	Ser	Val	Leu	Asp	Leu	Ala	Phe	Ser	Phe
	130					135					140				
Ile	Phe	Leu	Ala	Val	Met	Trp	Tyr	Tyr	Ser	Ser	Thr	Leu	Thr	Trp	Val
145					150					155					160
Val	Leu	Ala	Ser	Leu	Ile	Cys	Ile	Cys	Ala	Asn	Arg	Thr	Val	Leu	Ile
				165					170					175	
Ile	Ala	His	Arg	Leu	Ser	Thr	Val	Lys	Thr	Ala	His	Arg	Ile	Ile	Ala
		180						185					190		
Met	Asp	Lys	Gly	Arg	Ile	Val	Glu	Ala	Gly	Thr	Gln	Gln	Glu	Leu	Leu
	195						200					205			
Ala	Asn	Xaa	Asn	Gly	Tyr	Tyr	Arg	Tyr	Leu	Tyr	Asp	Leu	Gln		
	210					215					220				

<210> 175
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 <212> PRT
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 <223> Description of Artificial Sequence: overlap identity

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<400> 175
 Lys Phe Asp Phe Thr Trp Phe Ile Pro Ala Val Ile Lys Tyr Arg Xaa
 1 5 10 15
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 20 25 30
 Xaa Ile Thr Pro Leu Phe Phe Gln Val Val Met Asp Lys Val Leu Val
 35 40 45
 His Arg Gly Phe Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 50 55 60
 Xaa Xaa Xaa Phe Glu Ile Xaa Leu Gly Gly Leu Arg Thr Tyr Xaa Phe
 65 70 75 80
 Ala His Xaa Thr Ser Arg Ile Asp Val Glu Leu Gly Ala Arg Leu Phe
 85 90 95
 Arg His Leu Leu Xaa Leu Pro Xaa Ser Tyr Phe Glu Xaa Arg Arg Val
 100 105 110
 Gly Asp Thr Val Ala Arg Val Arg Glu Leu Xaa Gln Ile Arg Asn Phe
 115 120 125
 Leu Thr Gly Gln Ala Leu Thr Ser Xaa Leu Asp Leu Xaa Phe Ser Phe
 130 135 140
 Ile Phe Xaa Ala Val Met Trp Tyr Tyr Ser Xaa Xaa Leu Thr Xaa Val
 145 150 155 160
 Val Leu Xaa Ser Leu Xaa Cys Ile Cys Xaa Asn Arg Thr Val Leu Ile
 165 170 175
 Ile Ala His Arg Leu Ser Thr Val Lys Xaa Ala Xaa Arg Ile Ile Xaa
 180 185 190
 Met Asp Lys Gly Xaa Ile Xaa Glu Xaa Gly Xaa Xaa Gln Glu Leu Leu
 195 200 205
 Xaa Xaa Xaa Xaa Gly Xaa Tyr Xaa Tyr Leu Xaa Xaa Leu Gln
 210 215 220

<210> 176
 <211> 222
 <212> PRT
 <213> Artificial Sequence

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<223> Description of Artificial Sequence: HlyB

<400> 176

Lys Phe Asp Phe Thr Trp Phe Ile Pro Ala Val Ile Lys Tyr Arg Lys
1 5 10 15

Ile Phe Ile Glu Thr Leu Ile Val Ser Ile Phe Leu Gln Ile Phe Ala
20 25 30

Leu Ile Thr Pro Leu Phe Phe Gln Val Val Met Asp Lys Val Leu Val
35 40 45

His Arg Gly Phe Ser Thr Leu Asn Val Ile Thr Val Ala Leu Ala Ile
50 55 60

Val Val Leu Phe Glu Ile Ile Leu Gly Gly Leu Arg Thr Tyr Val Phe
65 70 75 80

Ala His Ser Thr Ser Arg Ile Asp Val Glu Leu Gly Ala Arg Leu Phe
85 90 95

Arg His Leu Leu Ala Leu Pro Ile Ser Tyr Phe Glu Ala Arg Arg Val
100 105 110

Gly Asp Thr Val Ala Arg Val Arg Glu Leu Asp Gln Ile Arg Asn Phe
115 120 125

Leu Thr Gly Gln Ala Leu Thr Ser Ile Leu Asp Leu Leu Phe Ser Phe
130 135 140

Ile Phe Phe Ala Val Met Trp Tyr Tyr Ser Pro Lys Leu Thr Leu Val
145 150 155 160

Val Leu Gly Ser Leu Pro Cys Ile Cys Gln Asn Arg Thr Val Leu Ile
165 170 175

Ile Ala His Arg Leu Ser Thr Val Lys Asn Ala Asp Arg Ile Ile Val
180 185 190

Met Asp Lys Gly Glu Ile Ile Glu Gln Gly Lys His Gln Glu Leu Leu
195 200 205

Lys Asp Glu Lys Gly Leu Tyr Ser Tyr Leu His Gln Leu Gln
210 215 220

<210> 177

<211> 240

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: ORF112a

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 <222> (77)
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<220>
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 <222> (87)
 <223> place-holder

<220>
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 <222> (223)
 <223> place-holder

<400> 177
 Met Asn Leu Ile Ser Arg Tyr Ile Ile Arg Gln Met Ala Val Met Ala
 1 5 10 15
 Val Tyr Ala Leu Leu Ala Phe Leu Ala Leu Tyr Ser Phe Phe Glu Ile
 20 25 30
 Leu Tyr Glu Thr Gly Asn Leu Gly Lys Gly Ser Tyr Gly Ile Trp Glu
 35 40 45
 Met Xaa Gly Tyr Thr Ala Leu Lys Met Xaa Ala Arg Ala Tyr Glu Leu
 50 55 60
 Met Pro Leu Ala Val Leu Ile Gly Gly Leu Val Ser Xaa Ser Gln Leu
 65 70 75 80
 Ala Ala Gly Ser Glu Leu Xaa Val Ile Lys Ala Ser Gly Met Ser Thr
 85 90 95
 Lys Lys Leu Leu Leu Ile Leu Ser Gln Phe Gly Phe Ile Phe Ala Ile
 100 105 110
 Ala Thr Val Ala Leu Gly Glu Trp Val Ala Pro Thr Leu Ser Gln Lys
 115 120 125
 Ala Glu Asn Ile Lys Ala Ala Ala Ile Asn Gly Lys Ile Ser Thr Gly
 130 135 140
 Asn Thr Gly Leu Trp Leu Lys Glu Lys Asn Ser Ile Ile Asn Val Arg
 145 150 155 160
 Glu Met Leu Pro Asp His Thr Leu Leu Gly Ile Lys Ile Trp Ala Arg
 165 170 175

Asn	Asp	Lys	Asn	Glu	Leu	Ala	Glu	Ala	Val	Glu	Ala	Asp	Ser	Ala	Val
			180					185					190		
Leu	Asn	Ser	Asp	Gly	Ser	Trp	Gln	Leu	Lys	Asn	Ile	Arg	Arg	Ser	Thr
		195					200					205			
Leu	Gly	Glu	Asp	Lys	Val	Glu	Val	Ser	Ile	Ala	Ala	Glu	Glu	Xaa	Trp
	210					215					220				
Pro	Ile	Ser	Val	Lys	Arg	Asn	Leu	Met	Asp	Val	Leu	Leu	Val	Lys	Pro
225					230					235					240

<210> 178
 <211> 360
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: ORF114a

<220>
 <221> SITE
 <222> (68)..(73)
 <223> place-holder

<220>
 <221> SITE
 <222> (85)
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<220>
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 <222> (296)
 <223> place-holder

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<400> 178															
Met	Asn	Lys	Gly	Leu	His	Arg	Ile	Ile	Phe	Ser	Lys	Lys	His	Ser	Thr
1				5					10					15	
Met	Val	Ala	Val	Ala	Glu	Thr	Ala	Asn	Ser	Gln	Gly	Lys	Gly	Lys	Gln
			20					25					30		
Ala	Gly	Ser	Ser	Val	Ser	Val	Ser	Leu	Lys	Thr	Ser	Gly	Asp	Leu	Cys
		35					40					45			

Gly Lys Leu Lys Thr Thr Leu Lys Thr Leu Val Cys Ser Leu Val Ser
 50 55 60
 Leu Ser Met Xaa Xaa Xaa Xaa Xaa Xaa Gln Ile Thr Thr Asp Lys Ser
 65 70 75 80
 Ala Pro Lys Asn Xaa Gln Val Val Ile Leu Lys Thr Asn Thr Gly Ala
 85 90 95
 Pro Leu Val Asn Ile Gln Thr Pro Asn Gly Arg Gly Leu Ser His Asn
 100 105 110
 Arg Tyr Thr Gln Phe Asp Val Asp Asn Lys Gly Ala Val Leu Asn Asn
 115 120 125
 Asp Arg Asn Asn Asn Pro Phe Leu Val Lys Gly Ser Ala Gln Leu Ile
 130 135 140
 Leu Asn Glu Val Arg Gly Thr Ala Ser Lys Leu Asn Gly Ile Val Thr
 145 150 155 160
 Val Gly Gly Gln Lys Ala Asp Val Ile Ile Ala Asn Pro Asn Gly Ile
 165 170 175
 Thr Val Asn Gly Gly Gly Phe Lys Asn Val Gly Arg Gly Ile Leu Thr
 180 185 190
 Ile Gly Ala Pro Gln Ile Gly Lys Asp Gly Ala Leu Thr Gly Phe Asp
 195 200 205
 Val Arg Gln Gly Thr Leu Thr Val Gly Ala Ala Gly Trp Asn Asp Lys
 210 215 220
 Gly Gly Ala Asp Tyr Thr Gly Val Leu Ala Arg Ala Val Ala Leu Gln
 225 230 235 240
 Gly Lys Leu Gln Gly Lys Asn Leu Ala Val Ser Thr Gly Pro Gln Lys
 245 250 255
 Val Asp Tyr Ala Ser Gly Glu Ile Ser Ala Gly Thr Ala Ala Gly Thr
 260 265 270
 Lys Pro Thr Ile Ala Leu Asp Thr Ala Ala Leu Gly Gly Met Tyr Ala
 275 280 285
 Asp Ser Ile Thr Leu Ile Ala Xaa Glu Lys Gly Val Gly Val Lys Asn
 290 295 300
 Ala Gly Thr Leu Glu Ala Ala Lys Gln Leu Ile Val Thr Ser Ser Gly
 305 310 315 320
 Arg Ile Glu Asn Ser Gly Arg Ile Ala Thr Thr Ala Asp Gly Thr Glu
 325 330 335
 Ala Ser Pro Thr Tyr Leu Xaa Ile Glu Thr Thr Glu Lys Gly Ala Xaa
 340 345 350
 Gly Thr Phe Ile Ser Asn Gly Gly

355

360

<210> 179

<211> 1574

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: ORF114-1

<400> 179

Met	Asn	Lys	Gly	Leu	His	Arg	Ile	Ile	Phe	Ser	Lys	Lys	His	Ser	Thr
1				5					10					15	

Met	Val	Ala	Val	Ala	Glu	Thr	Ala	Asn	Ser	Gln	Gly	Lys	Gly	Lys	Gln
			20					25					30		

Ala	Gly	Ser	Ser	Val	Ser	Val	Ser	Leu	Lys	Thr	Ser	Gly	Asp	Leu	Cys
		35					40					45			

Gly	Lys	Leu	Lys	Thr	Thr	Leu	Lys	Thr	Leu	Val	Cys	Ser	Leu	Val	Ser
50						55					60				

Leu	Ser	Met	Val	Leu	Pro	Ala	His	Ala	Gln	Ile	Thr	Thr	Asp	Lys	Ser
65					70					75					80

Ala	Pro	Lys	Asn	Gln	Gln	Val	Val	Ile	Leu	Lys	Thr	Asn	Thr	Gly	Ala
				85					90					95	

Pro	Leu	Val	Asn	Ile	Gln	Thr	Pro	Asn	Gly	Arg	Gly	Leu	Ser	His	Asn
			100					105					110		

Arg	Tyr	Thr	Gln	Phe	Asp	Val	Asp	Asn	Lys	Gly	Ala	Val	Leu	Asn	Asn
		115					120					125			

Asp	Arg	Asn	Asn	Asn	Pro	Phe	Val	Val	Lys	Gly	Ser	Ala	Gln	Leu	Ile
130						135					140				

Leu	Asn	Glu	Val	Arg	Gly	Thr	Ala	Ser	Lys	Leu	Asn	Gly	Ile	Val	Thr
145					150					155					160

Val	Gly	Gly	Gln	Lys	Ala	Asp	Val	Ile	Ile	Ala	Asn	Pro	Asn	Gly	Ile
			165						170					175	

Thr	Val	Asn	Gly	Gly	Gly	Phe	Lys	Asn	Val	Gly	Arg	Gly	Ile	Leu	Thr
		180					185						190		

Thr	Gly	Ala	Pro	Gln	Ile	Gly	Lys	Asp	Gly	Ala	Leu	Thr	Gly	Phe	Asp
	195					200						205			

Val	Arg	Gln	Gly	Thr	Leu	Thr	Val	Gly	Ala	Ala	Gly	Trp	Asn	Asp	Lys
	210					215					220				

Gly	Gly	Ala	Asp	Tyr	Thr	Gly	Val	Leu	Ala	Arg	Ala	Val	Ala	Leu	Gln
225					230					235					240

Gly Lys Leu Gln Gly Lys Asn Leu Ala Val Ser Thr Gly Pro Gln Lys
 245 250 255
 Val Asp Tyr Ala Ser Gly Glu Ile Ser Ala Gly Thr Ala Ala Gly Thr
 260 265 270
 Lys Pro Thr Ile Ala Leu Asp Thr Ala Ala Leu Gly Gly Met Tyr Ala
 275 280 285
 Asp Ser Ile Thr Leu Ile Ala Asn Glu Lys Gly Val Gly Val Lys Asn
 290 295 300
 Ala Gly Thr Leu Glu Ala Ala Lys Gln Leu Ile Val Thr Ser Ser Gly
 305 310 315 320
 Arg Ile Glu Asn Ser Gly Arg Ile Ala Thr Thr Ala Asp Gly Thr Glu
 325 330 335
 Ala Ser Pro Thr Tyr Leu Ser Ile Glu Thr Thr Glu Lys Gly Ala Ala
 340 345 350
 Gly Thr Phe Ile Ser Asn Gly Gly Arg Ile Glu Ser Lys Gly Leu Leu
 355 360 365
 Val Ile Glu Thr Gly Glu Asp Ile Ser Leu Arg Asn Gly Ala Val Val
 370 375 380
 Gln Asn Asn Gly Ser Arg Pro Ala Thr Thr Val Leu Asn Ala Gly His
 385 390 395 400
 Asn Leu Val Ile Glu Ser Lys Thr Asn Val Asn Asn Ala Lys Gly Pro
 405 410 415
 Ala Thr Leu Ser Ala Asp Gly Arg Thr Val Ile Lys Glu Ala Ser Ile
 420 425 430
 Gln Thr Gly Thr Thr Val Tyr Ser Ser Ser Lys Gly Asn Ala Glu Leu
 435 440 445
 Gly Asn Asn Thr Arg Ile Thr Gly Ala Asp Val Thr Val Leu Ser Asn
 450 455 460
 Gly Thr Ile Ser Ser Ser Ala Val Ile Asp Ala Lys Asp Thr Ala His
 465 470 475 480
 Ile Glu Ala Gly Lys Pro Leu Ser Leu Glu Ala Ser Thr Val Thr Ser
 485 490 495
 Asp Ile Arg Leu Asn Gly Gly Ser Ile Lys Gly Gly Lys Gln Leu Ala
 500 505 510
 Leu Leu Ala Asp Asp Asn Ile Thr Ala Lys Thr Thr Asn Leu Asn Thr
 515 520 525
 Pro Gly Asn Leu Tyr Val His Thr Gly Lys Asp Leu Asn Leu Asn Val
 530 535 540

Asp	Lys	Asp	Leu	Ser	Ala	Ala	Ser	Ile	His	Leu	Lys	Ser	Asp	Asn	Ala	
545					550					555					560	
Ala	His	Ile	Thr	Gly	Thr	Ser	Lys	Thr	Leu	Thr	Ala	Ser	Lys	Asp	Met	
				565					570					575		
Gly	Val	Glu	Ala	Gly	Ser	Leu	Asn	Val	Thr	Asn	Thr	Asn	Leu	Arg	Thr	
			580					585					590			
Asn	Ser	Gly	Asn	Leu	His	Ile	Gln	Ala	Ala	Lys	Gly	Asn	Ile	Gln	Leu	
		595					600					605				
Arg	Asn	Thr	Lys	Leu	Asn	Ala	Ala	Lys	Ala	Leu	Glu	Thr	Thr	Ala	Leu	
	610					615					620					
Gln	Gly	Asn	Ile	Val	Ser	Asp	Gly	Leu	His	Ala	Val	Ser	Ala	Asp	Gly	
625					630					635					640	
His	Val	Ser	Leu	Leu	Ala	Asn	Gly	Asn	Ala	Asp	Phe	Thr	Gly	His	Asn	
				645					650					655		
Thr	Leu	Thr	Ala	Lys	Ala	Asp	Val	Asn	Ala	Gly	Ser	Val	Gly	Lys	Gly	
			660					665					670			
Arg	Leu	Lys	Ala	Asp	Asn	Thr	Asn	Ile	Thr	Ser	Ser	Ser	Gly	Asp	Ile	
		675					680						685			
Thr	Leu	Val	Ala	Gly	Asn	Gly	Ile	Gln	Leu	Gly	Asp	Gly	Lys	Gln	Arg	
	690					695					700					
Asn	Ser	Ile	Asn	Gly	Lys	His	Ile	Ser	Ile	Lys	Asn	Asn	Gly	Gly	Asn	
705					710					715					720	
Ala	Asp	Leu	Lys	Asn	Leu	Asn	Val	His	Ala	Lys	Ser	Gly	Ala	Leu	Asn	
				725					730					735		
Ile	His	Ser	Asp	Arg	Ala	Leu	Ser	Ile	Glu	Asn	Thr	Lys	Leu	Glu	Ser	
			740					745					750			
Thr	His	Asn	Thr	His	Leu	Asn	Ala	Gln	His	Glu	Arg	Val	Thr	Leu	Asn	
		755					760					765				
Gln	Val	Asp	Ala	Tyr	Ala	His	Arg	His	Leu	Ser	Ile	Thr	Gly	Ser	Gln	
	770					775					780					
Ile	Trp	Gln	Asn	Asp	Lys	Leu	Pro	Ser	Ala	Asn	Lys	Leu	Val	Ala	Asn	
785					790					795					800	
Gly	Val	Leu	Ala	Leu	Asn	Ala	Arg	Tyr	Ser	Gln	Ile	Ala	Asp	Asn	Thr	
				805					810					815		
Thr	Leu	Arg	Ala	Gly	Ala	Ile	Asn	Leu	Thr	Ala	Gly	Thr	Ala	Leu	Val	
			820					825					830			
Lys	Arg	Gly	Asn	Ile	Asn	Trp	Ser	Thr	Val	Ser	Thr	Lys	Thr	Leu	Glu	
		835					840					845				

Asp Asn Ala Glu Leu Lys Pro Leu Ala Gly Arg Leu Asn Ile Glu Ala
 850 855 860
 Gly Ser Gly Thr Leu Thr Ile Glu Pro Ala Asn Arg Ile Ser Ala His
 865 870 875 880
 Thr Asp Leu Ser Ile Lys Thr Gly Gly Lys Leu Leu Leu Ser Ala Lys
 885 890 895
 Gly Gly Asn Ala Gly Ala Pro Ser Ala Gln Val Ser Ser Leu Glu Ala
 900 905 910
 Lys Gly Asn Ile Arg Leu Val Thr Gly Glu Thr Asp Leu Arg Gly Ser
 915 920 925
 Lys Ile Thr Ala Gly Lys Asn Leu Val Val Ala Thr Thr Lys Gly Lys
 930 935 940
 Leu Asn Ile Glu Ala Val Asn Asn Ser Phe Ser Asn Tyr Phe Pro Thr
 945 950 955 960
 Gln Lys Ala Ala Glu Leu Asn Gln Lys Ser Lys Glu Leu Glu Gln Gln
 965 970 975
 Ile Ala Gln Leu Lys Lys Ser Ser Pro Lys Ser Lys Leu Ile Pro Thr
 980 985 990
 Leu Gln Glu Glu Arg Asp Arg Leu Ala Phe Tyr Ile Gln Ala Ile Asn
 995 1000 1005
 Lys Glu Val Lys Gly Lys Lys Pro Lys Gly Lys Glu Tyr Leu Gln Ala
 1010 1015 1020
 Lys Leu Ser Ala Gln Asn Ile Asp Leu Ile Ser Ala Gln Gly Ile Glu
 1025 1030 1035 1040
 Ile Ser Gly Ser Asp Ile Thr Ala Ser Lys Lys Leu Asn Leu His Ala
 1045 1050 1055
 Ala Gly Val Leu Pro Lys Ala Ala Asp Ser Glu Ala Ala Ala Ile Leu
 1060 1065 1070
 Ile Asp Gly Ile Thr Asp Gln Tyr Glu Ile Gly Lys Pro Thr Tyr Lys
 1075 1080 1085
 Ser His Tyr Asp Lys Ala Ala Leu Asn Lys Pro Ser Arg Leu Thr Gly
 1090 1095 1100
 Arg Thr Gly Val Ser Ile His Ala Ala Ala Leu Asp Asp Ala Arg
 1105 1110 1115 1120
 Ile Ile Ile Gly Ala Ser Glu Ile Lys Ala Pro Ser Gly Ser Ile Asp
 1125 1130 1135
 Ile Lys Ala His Ser Asp Ile Val Leu Glu Ala Gly Gln Asn Asp Ala
 1140 1145 1150
 Tyr Thr Phe Leu Lys Thr Lys Gly Lys Ser Gly Lys Ile Ile Arg Lys

1155	1160	1165
Thr Lys Phe Thr Ser Thr Arg Asp His Leu Ile Met Pro Ala Pro Val 1170	1175	1180
Glu Leu Thr Ala Asn Gly Ile Thr Leu Gln Ala Gly Gly Asn Ile Glu 1185	1190	1195 1200
Ala Asn Thr Thr Arg Phe Asn Ala Pro Ala Gly Lys Val Thr Leu Val 1205	1210	1215
Ala Gly Glu Glu Leu Gln Leu Leu Ala Glu Glu Gly Ile His Lys His 1220	1225	1230
Glu Leu Asp Val Gln Lys Ser Arg Arg Phe Ile Gly Ile Lys Val Gly 1235	1240	1245
Lys Ser Asn Tyr Ser Lys Asn Glu Leu Asn Glu Thr Lys Leu Pro Val 1250	1255	1260
Arg Val Val Ala Gln Thr Ala Ala Thr Arg Ser Gly Trp Asp Thr Val 1265	1270	1275 1280
Leu Glu Gly Thr Glu Phe Lys Thr Thr Leu Ala Gly Ala Asp Ile Gln 1285	1290	1295
Ala Gly Val Gly Glu Lys Ala Arg Ala Asp Ala Lys Ile Ile Leu Lys 1300	1305	1310
Gly Ile Val Asn Arg Ile Gln Ser Glu Glu Lys Leu Glu Thr Asn Ser 1315	1320	1325
Thr Val Trp Gln Lys Gln Ala Gly Arg Gly Ser Thr Ile Glu Thr Leu 1330	1335	1340
Lys Leu Pro Ser Phe Glu Ser Pro Thr Pro Pro Lys Leu Thr Ala Pro 1345	1350	1355 1360
Gly Gly Tyr Ile Val Asp Ile Pro Lys Gly Asn Leu Lys Thr Glu Ile 1365	1370	1375
Glu Lys Leu Ala Lys Gln Pro Glu Tyr Ala Tyr Leu Lys Gln Leu Gln 1380	1385	1390
Val Ala Lys Asn Val Asn Trp Asn Gln Val Gln Leu Ala Tyr Asp Lys 1395	1400	1405
Trp Asp Tyr Lys Gln Glu Gly Leu Thr Arg Ala Gly Ala Ala Ile Val 1410	1415	1420
Thr Ile Ile Val Thr Ala Leu Thr Tyr Gly Tyr Gly Ala Thr Ala Ala 1425	1430	1435 1440
Gly Gly Val Ala Ala Ser Gly Ser Ser Thr Ala Ala Ala Ala Gly Thr 1445	1450	1455
Ala Ala Thr Thr Thr Ala Ala Ala Thr Thr Val Ser Thr Ala Thr Ala 1460	1465	1470

Met Gln Thr Ala Ala Leu Ala Ser Leu Tyr Ser Gln Ala Ala Val Ser
1475 1480 1485

Ile Ile Asn Asn Lys Gly Asp Val Gly Lys Ala Leu Lys Asp Leu Gly
1490 1495 1500

Thr Ser Asp Thr Val Lys Gln Ile Val Thr Ser Ala Leu Thr Ala Gly
1505 1510 1515 1520
Ala Leu Asn Gln Met Gly Ala Asp Ile Ala Gln Leu Asn Ser Lys Val
1525 1530 1535

Arg Thr Glu Leu Phe Ser Ser Thr Gly Asn Gln Thr Ile Ala Asn Leu
1540 1545 1550

Gly Gly Arg Leu Ala Thr Asn Leu Ser Asn Ala Gly Ile Ser Ala Gly
1555 1560 1565

Ile Asn Thr Ala Val Asn
1570

<210> 180
<211> 281
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: ORF114

<220>
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<222> (29)..(51)
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<220>
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<220>
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<222> (229)

<223> place-holder

<400> 180

Ala Val Ala Glu Thr Ala Asn Ser Gln Gly Lys Gly Lys Gln Ala Gly
1 5 10 15

Ser Ser Val Ser Val Ser Leu Lys Thr Ser Gly Asp Xaa Xaa Xaa Xaa
20 25 30

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
35 40 45

Xaa Xaa Xaa Pro Ala His Ala Gln Ile Thr Thr Asp Lys Ser Ala Pro
50 55 60

Lys Asn Gln Gln Val Val Ile Leu Lys Thr Asn Thr Gly Ala Pro Leu
65 70 75 80

Val Asn Ile Gln Thr Pro Asn Gly Arg Gly Leu Ser His Asn Arg Xaa
85 90 95

Tyr Ala Phe Asp Val Asp Asn Lys Gly Ala Val Leu Asn Asn Asp Arg
100 105 110

Asn Asn Asn Pro Phe Val Val Lys Gly Ser Ala Gln Leu Ile Leu Asn
115 120 125

Glu Val Arg Gly Thr Ala Ser Lys Leu Asn Gly Ile Val Thr Val Gly
130 135 140

Gly Gln Lys Ala Asp Val Ile Ile Ala Asn Pro Asn Gly Ile Thr Val
145 150 155 160

Asn Gly Gly Gly Phe Lys Asn Val Gly Arg Gly Ile Leu Thr Thr Gly
165 170 175

Ala Pro Gln Ile Gly Lys Asp Gly Ala Leu Thr Gly Phe Asp Val Val
180 185 190

Lys Ala His Trp Thr Val Xaa Ala Ala Gly Trp Asn Asp Lys Gly Gly
195 200 205

Ala Xaa Tyr Thr Gly Val Leu Ala Arg Ala Val Ala Leu Gln Gly Lys
210 215 220

Xaa Xaa Gly Lys Xaa Leu Ala Val Ser Thr Gly Pro Gln Lys Val Asp
225 230 235 240

Tyr Ala Ser Gly Glu Ile Ser Ala Gly Thr Ala Ala Gly Thr Lys Pro
245 250 255

Thr Ile Ala Leu Asp Thr Ala Ala Leu Gly Gly Met Tyr Ala Asp Ser
260 265 270

Ile Thr Leu Ile Ala Asn Glu Lys Gly
275 280

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 20 25 30
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 35 40 45
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Pro Ala Xaa Ala Xaa Xaa Ile Xaa Xaa
 50 55 60
 Asp Lys Ser Ala Pro Lys Asn Gln Gln Xaa Val Ile Leu Xaa Thr Xaa
 65 70 75 80
 Xaa Gly Xaa Pro Xaa Val Asn Ile Gln Thr Pro Xaa Xaa Xaa Gly Xaa
 85 90 95
 Ser Xaa Asn Arg Xaa Xaa Xaa Phe Asp Val Asp Xaa Lys Gly Xaa Xaa
 100 105 110
 Leu Asn Asn Xaa Arg Xaa Asn Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 115 120 125
 Xaa Xaa Asn Pro Xaa Xaa Xaa Xaa Gly Xaa Ala Xaa Xaa Ile Xaa Asn
 130 135 140
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Ser Xaa Leu Asn Gly Xaa Xaa Xaa Val
 145 150 155 160
 Gly Gly Xaa Xaa Ala Xaa Val Xaa Xaa Ala Asn Pro Xaa Gly Ile Xaa
 165 170 175
 Val Asn Gly Gly Gly Xaa Xaa Asn Xaa Xaa Xaa Xaa Xaa Leu Thr Xaa
 180 185 190
 Gly Xaa Pro Xaa Xaa Xaa Xaa Xaa Gly Xaa Leu Thr Gly Phe Asp Val
 195 200 205
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Gly Xaa Xaa Asp Xaa Xaa
 210 215 220
 Xaa Ala Xaa Tyr Thr Xaa Xaa Leu Xaa Arg Ala Xaa Xaa Xaa Xaa Xaa

225 230 235 240
 Xaa Xaa Xaa Gly Lys Xaa Xaa Xaa Val Xaa Xaa Gly Xaa Xaa Lys Xaa
 245 250 255
 Asp Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Ala Xaa Xaa Xaa Xaa
 260 265 270
 Xaa Xaa Xaa Xaa Pro Thr Xaa Ala Xaa Asp Thr Ala Xaa Leu Gly Gly
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 Met Tyr Ala Asp Xaa Ile Thr Leu Ile Xaa Xaa Xaa Xaa Gly
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 35 40 45
 Leu Gly Val Ala Ala Phe Ser Pro Ala Pro Ala Ser Gly Ile Ile Ala
 50 55 60
 Asp Lys Ser Ala Pro Lys Asn Gln Gln Ala Val Ile Leu Gln Thr Ala
 65 70 75 80
 Asn Gly Leu Pro Gln Val Asn Ile Gln Thr Pro Ser Ser Gln Gly Val
 85 90 95
 Ser Val Asn Arg Phe Lys Gln Phe Asp Val Asp Glu Lys Gly Val Ile
 100 105 110
 Leu Asn Asn Ser Arg Ser Asn Thr Gln Thr Gln Leu Gly Gly Trp Ile
 115 120 125
 Gln Gly Asn Pro His Leu Ala Arg Gly Glu Ala Arg Val Ile Val Asn
 130 135 140
 Gln Ile Asp Ser Ser Asn Pro Ser Leu Leu Asn Gly Tyr Ile Glu Val
 145 150 155 160
 Gly Gly Lys Arg Ala Glu Val Val Val Ala Asn Pro Ser Gly Ile Arg
 165 170 175

Val	Asn	Gly	Gly	Gly	Leu	Ile	Asn	Ala	Ala	Ser	Val	Thr	Leu	Thr	Ser
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Gly	Val	Pro	Val	Leu	Asn	Asn	Gly	Asn	Leu	Thr	Gly	Phe	Asp	Val	Ser
		195					200					205			
Ser	Gly	Lys	Val	Val	Ile	Gly	Gly	Lys	Gly	Leu	Asp	Thr	Ser	Asp	Ala
	210					215					220				
Asp	Tyr	Thr	Arg	Ile	Leu	Ser	Arg	Ala	Ala	Glu	Ile	Asn	Ala	Gly	Val
225					230					235					240
Trp	Gly	Lys	Asp	Val	Lys	Val	Val	Ser	Gly	Lys	Asn	Lys	Leu	Asp	Phe
			245						250					255	
Asp	Gly	Ser	Leu	Ala	Lys	Thr	Ala	Ser	Ala	Pro	Ser	Ser	Ser	Asp	Ser
			260					265						270	
Val	Thr	Pro	Thr	Val	Ala	Ile	Asp	Thr	Ala	Thr	Leu	Gly	Gly	Met	Tyr
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 Ala Gly Ser Ser Val Ser Val Ser Leu Lys Thr Ser Gly Asp Xaa Xaa
 35 40 45
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 50 55 60
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Gln Ile Thr Thr Asp Lys Ser
 65 70 75 80
 Ala Pro Lys Asn Xaa Gln Val Val Ile Leu Lys Thr Asn Thr Gly Ala
 85 90 95
 Pro Leu Val Asn Ile Gln Thr Pro Asn Gly Arg Gly Leu Ser His Asn
 100 105 110
 Arg Tyr Thr Gln Phe Asp Val Asp Asn Lys Gly Ala Val Leu Asn Asn
 115 120 125
 Asp Arg Asn Asn Asn Pro Phe Leu Val Lys Gly Ser Ala Gln Leu Ile
 130 135 140
 Leu Asn Glu Val Arg Gly Thr Ala Ser Lys Leu Asn Gly Ile Val Thr
 145 150 155 160
 Val Gly Gly Gln Lys Ala Asp Val Ile Ile Ala Asn Pro Asn Gly Ile
 165 170 175
 Thr Val Asn Gly Gly Gly Phe Lys Asn Val Gly Arg Gly Ile Leu Thr
 180 185 190

Ile	Gly	Ala	Pro	Gln	Ile	Gly	Lys	Asp	Gly	Ala	Leu	Thr	Gly	Phe	Asp		
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Gly	Gly	Ala	Asp	Tyr	Thr	Gly	Val	Leu	Ala	Arg	Ala	Val	Ala	Leu	Gln		
225					230					235					240		
Gly	Lys	Leu	Gln	Gly	Lys	Asn	Leu	Ala	Val	Ser	Thr	Gly	Pro	Gln	Lys		
			245						250					255			
Val	Asp	Tyr	Ala	Ser	Gly	Glu	Ile	Ser	Ala	Gly	Thr	Ala	Ala	Gly	Thr		
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Lys	Pro	Thr	Ile	Ala	Leu	Asp	Thr	Ala	Ala	Leu	Gly	Gly	Met	Tyr	Ala		
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Asp	Ser	Ile	Thr	Leu	Ile	Ala	Xaa	Glu	Lys	Gly	Val	Gly	Val	Lys	Asn		
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Arg	Ile	Glu	Asn	Ser	Gly	Arg	Ile	Ala	Thr	Thr	Ala	Asp	Gly	Thr	Glu		
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Ala	Ser	Pro	Thr	Tyr	Leu	Xaa	Ile	Glu	Thr	Thr	Glu	Lys	Gly	Ala	Xaa		
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Val	Ile	Glu	Thr	Gly	Glu	Asp	Ile	Xaa	Leu	Arg	Asn	Gly	Ala	Val	Val		
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Gln	Asn	Asn	Gly	Ser	Arg	Pro	Ala	Thr	Thr	Val	Leu	Asn	Ala	Gly	His		
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			405						410					415			
Xaa	Asn	Leu	Ser	Ala	Gly	Gly	Arg	Thr	Thr	Ile	Asn	Asp	Ala	Thr	Ile		
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Gly	Ser	Ile	Gly	Ser	Ala	Ala	Val	Ile	Glu	Ala	Lys	Asp	Thr	Ala	His		
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Met Asn Lys Xaa Xaa Xaa Xaa Xaa Ile Phe Xaa Lys Lys Xaa Ser Xaa
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Met Xaa Ala Val Ala Glu Xaa Xaa Xaa Xaa Xaa Gly Lys Xaa Xaa Gln
20 25 30

Xaa Xaa Xaa Xaa Xaa Ser Val Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
35 40 45

Ser Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
50 55 60

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Ile
65 70 75 80

Xaa Xaa Asp Lys Ser Ala Pro Lys Asn Xaa Gln Xaa Val Ile Leu Xaa
85 90 95

Thr Xaa Xaa Gly Xaa Pro Xaa Val Asn Ile Gln Thr Pro Xaa Xaa Xaa
100 105 110

Gly Xaa Ser Xaa Asn Arg Xaa Xaa Gln Phe Asp Val Asp Xaa Lys Gly
115 120 125

Xaa Xaa Leu Asn Asn Xaa Arg Xaa Asn Xaa Xaa Xaa Xaa Xaa Xaa Xaa
130 135 140

Xaa Xaa Xaa Xaa Asn Pro Xaa Leu Xaa Xaa Gly Xaa Ala Xaa Xaa Ile
145 150 155 160

Xaa Asn Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Ser Xaa Leu Asn Gly Xaa Xaa
165 170 175

Xaa Val Gly Gly Xaa Xaa Ala Xaa Val Xaa Xaa Ala Asn Pro Xaa Gly
180 185 190

Ile Xaa Val Asn Gly Gly Gly Xaa Xaa Asn Xaa Xaa Xaa Xaa Xaa Leu
195 200 205

Thr Xaa Gly Xaa Pro Xaa Xaa Xaa Xaa Xaa Gly Xaa Leu Thr Gly Phe
210 215 220

Asp Val Xaa Xaa Gly Xaa Xaa Xaa Xaa Gly Xaa Xaa Gly Xaa Xaa Asp
225 230 235 240

Xaa Xaa Xaa Ala Asp Tyr Thr Xaa Xaa Leu Xaa Arg Ala Xaa Xaa Xaa
245 250 255

Xaa Xaa Xaa Xaa Xaa Gly Lys Xaa Xaa Xaa Val Xaa Xaa Gly Xaa Xaa
260 265 270

Lys	Xaa	Asp	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Ala	Xaa	Xaa	
		275						280					285			
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Pro	Thr	Xaa	Ala	Xaa	Asp	Thr	Ala	Xaa	Leu	
		290					295					300				
Gly	Gly	Met	Tyr	Ala	Asp	Xaa	Ile	Thr	Leu	Ile	Xaa	Xaa	Xaa	Xaa	Gly	
305					310					315					320	
Xaa	Xaa	Xaa	Xaa	Asn	Xaa	Gly	Xaa	Xaa	Xaa	Ala	Ala	Xaa	Xaa	Xaa	Xaa	
				325						330					335	
Xaa	Xaa	Xaa	Xaa	Xaa	Gly	Xaa	Xaa	Xaa	Asn	Ser	Gly	Xaa	Ile	Xaa	Xaa	
				340					345				350			
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Ala	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Thr	
				355				360					365			
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Gly	Xaa	Ile	
				370				375					380			
Xaa	Ser	Xaa	Xaa	Xaa	Xaa	Val	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Ile	Xaa	Xaa	
385						390					395				400	
Xaa	Xaa	Gly	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Gly	Ser	Xaa	Xaa	Xaa	Xaa	Xaa	
				405					410						415	
Xaa	Xaa	Xaa	Xaa	Gly	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Ser	Xaa	Xaa	Xaa	Xaa	
				420					425					430		
Asn	Asn	Xaa	Xaa	Gly	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Ser	Xaa	Xaa	
		435						440					445			
Xaa	Xaa	Xaa	Xaa	Xaa	Asn	Asp	Xaa	Xaa	Xaa	Xaa	Ala	Xaa	Xaa	Xaa	Val	
		450				455					460					
Xaa	Ser	Xaa	Xaa	Xaa	Xaa	Asp	Xaa	Xaa	Xaa	Gly	Xaa	Xaa	Xaa	Xaa	Xaa	
465						470				475					480	
Xaa	Xaa	Xaa	Xaa	Xaa	Thr	Xaa	Xaa	Xaa	Xaa	Gly	Xaa	Xaa	Xaa	Xaa	Xaa	
				485						490					495	
Xaa	Xaa	Ile	Xaa	Ala	Xaa	Asp	Thr	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	
		500						505						510		
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Ser	Xaa	Xaa	Arg	Xaa	Xaa	Xaa	
		515						520				525				
Xaa	Xaa	Xaa	Xaa	Gly	Xaa	Xaa	Xaa	Xaa	Xaa	Leu	Xaa	Xaa	Xaa	Xaa	Xaa	
		530						535				540				
Ile	Thr	Xaa	Xaa	Xaa	Xaa	Xaa	Ala	Lys	Xaa	Xaa	Asn	Xaa	Xaa	Thr	Xaa	
545						550					555				560	
Gly	Xaa	Xaa	Tyr	Xaa	Xaa	Xaa	Gly	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Asp	
				565						570					575	

Xaa Xaa Leu Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Ala Ala
 580 585 590
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Ala Xaa Xaa Xaa Xaa Xaa
 595 600 605
 Xaa Xaa Ala Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 610 615 620
 Ser Gly Xaa Leu His Ile Xaa Xaa Ala Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 625 630 635 640
 Gln Xaa Xaa Asn Thr Xaa Leu Xaa Asn Xaa Xaa Xaa Ala Xaa Glu Xaa
 645 650 655
 Xaa Xaa Xaa Xaa Gly Asn Ile
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 <213> Artificial Sequence

<220>
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<400> 185
 Met Asn Lys Arg Cys Tyr Lys Val Ile Phe Asn Lys Lys Arg Ser Cys
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 Met Met Ala Val Ala Glu Asn Val His Arg Asp Gly Lys Ser Met Gln
 20 25 30
 Asp Ser Glu Ala Ala Ser Val Arg Val Thr Gly Ala Ala Ser Val Ser
 35 40 45
 Ser Ala Arg Ala Ala Phe Gly Phe Arg Met Ala Ala Phe Ser Val Met
 50 55 60
 Leu Ala Leu Gly Val Ala Ala Phe Ser Pro Ala Pro Ala Ser Gly Ile
 65 70 75 80
 Ile Ala Asp Lys Ser Ala Pro Lys Asn Gln Gln Ala Val Ile Leu Gln
 85 90 95
 Thr Ala Asn Gly Leu Pro Gln Val Asn Ile Gln Thr Pro Ser Ser Gln
 100 105 110
 Gly Val Ser Val Asn Arg Phe Lys Gln Phe Asp Val Asp Glu Lys Gly
 115 120 125
 Val Ile Leu Asn Asn Ser Arg Ser Asn Thr Gln Thr Gln Leu Gly Gly
 130 135 140
 Trp Ile Gln Gly Asn Pro His Leu Ala Arg Gly Glu Ala Arg Val Ile
 145 150 155 160

Val Asn Gln Ile Asp Ser Ser Asn Pro Ser Leu Leu Asn Gly Tyr Ile
 165 170 175
 Glu Val Gly Gly Lys Arg Ala Glu Val Val Val Ala Asn Pro Ser Gly
 180 185 190
 Ile Arg Val Asn Gly Gly Gly Leu Ile Asn Ala Ala Ser Val Thr Leu
 195 200 205
 Thr Ser Gly Val Pro Val Leu Asn Asn Gly Asn Leu Thr Gly Phe Asp
 210 215 220
 Val Ser Ser Gly Lys Val Val Ile Gly Gly Lys Gly Leu Asp Thr Ser
 225 230 235 240
 Asp Ala Asp Tyr Thr Arg Ile Leu Ser Arg Ala Ala Glu Ile Asn Ala
 245 250 255
 Gly Val Trp Gly Lys Asp Val Lys Val Val Ser Gly Lys Asn Lys Leu
 260 265 270
 Asp Phe Asp Gly Ser Leu Ala Lys Thr Ala Ser Ala Pro Ser Ser Ser
 275 280 285
 Asp Ser Val Thr Pro Thr Val Ala Ile Asp Thr Ala Thr Leu Gly Gly
 290 295 300
 Met Tyr Ala Asp Lys Ile Thr Leu Ile Ser Thr Asp Asn Gly Ala Val
 305 310 315 320
 Ile Arg Asn Lys Gly Arg Ile Phe Ala Ala Thr Gly Gly Val Thr Leu
 325 330 335
 Ser Ala Asp Gly Lys Leu Ser Asn Ser Gly Ser Ile Asp Ala Ala Glu
 340 345 350
 Ile Thr Ile Ser Ala Gln Thr Val Asp Asn Arg Gln Gly Phe Ile Arg
 355 360 365
 Ser Gly Lys Gly Ser Val Leu Lys Val Ser Asp Gly Ile Asn Asn Gln
 370 375 380
 Ala Gly Leu Ile Gly Ser Ala Gly Leu Leu Asp Ile Arg Asp Thr Gly
 385 390 395 400
 Lys Ser Ser Leu His Ile Asn Asn Thr Asp Gly Thr Ile Ile Ala Gly
 405 410 415
 Lys Asp Val Ser Leu Gln Ala Lys Ser Leu Asp Asn Asp Gly Ile Leu
 420 425 430
 Thr Ala Ala Arg Asp Val Ser Val Ser Leu His Asp Asp Phe Ala Gly
 435 440 445
 Lys Arg Asp Ile Glu Ala Gly Arg Thr Leu Thr Phe Ser Thr Gln Gly
 450 455 460

Arg Leu Lys Asn Thr Arg Ile Ile Gln Ala Gly Asp Thr Val Ser Leu
 465 470 475 480
 Thr Ala Ala Gln Ile Asp Asn Thr Val Ser Gly Lys Ile Gln Ser Gly
 485 490 495
 Asn Arg Thr Gly Leu Asn Gly Lys Asn Gly Ile Thr Asn Arg Gly Leu
 500 505 510
 Ile Asn Ser Asn Gly Ile Thr Leu Leu Gln Thr Glu Ala Lys Ser Asp
 515 520 525
 Asn Ala Gly Thr Gly Arg Ile Tyr Gly Ser Arg Val Ala Val Glu Ala
 530 535 540
 Asp Thr Leu Leu Asn Arg Glu Glu Thr Val Asn Gly Glu Thr Lys Ala
 545 550 555 560
 Ala Val Ile Ala Ala Arg Glu Arg Leu Asp Ile Gly Ala Arg Glu Ile
 565 570 575
 Glu Asn Arg Glu Ala Ala Leu Leu Ser Ser Ser Gly Asp Leu His Ile
 580 585 590
 Gly Ser Ala Leu Asn Gly Ser Arg Gln Val Gln Gly Ala Asn Thr Ser
 595 600 605
 Leu His Asn Arg Ser Ala Ala Ile Glu Ser Ser Gly Asn Ile
 610 615 620

<210> 186
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<220>
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<400> 186
Leu Gln Gly Lys Leu Gln Gly Lys Asn Leu Ala Val Ser Thr Gly Pro
1 5 10 15
Gln Lys Val Asp Tyr Ala Ser Gly Glu Ile Ser Ala Gly Thr Ala Ala
20 25 30
Gly Thr Lys Pro Thr Ile Ala Leu Asp Thr Ala Ala Leu Gly Gly Met
35 40 45
Tyr Ala Asp Ser Ile Thr Leu Ile Ala Xaa Glu Lys Gly Val Gly Val
50 55 60
Lys Asn Ala Gly Thr Leu Glu Ala Ala Lys Gln Leu Ile Val Thr Ser
65 70 75 80
Ser Gly Arg Ile Glu Asn Ser Gly Arg Ile Ala Thr Thr Ala Asp Gly
85 90 95
Thr Glu Ala Ser Pro Thr Tyr Leu Xaa Ile Glu Thr Thr Glu Lys Gly
100 105 110
Ala Xaa Gly Thr Phe Ile Ser Asn Gly Gly Arg Ile Glu Ser Lys Gly
115 120 125
Leu Leu Val Ile Glu Thr Gly Glu Asp Ile Xaa Leu Arg Asn Gly Ala
130 135 140
Val Val Gln Asn Asn Gly Ser Arg Pro Ala Thr Thr Val Leu Asn Ala
145 150 155 160
Gly His Asn Leu Val Ile Glu Ser Lys Thr Asn Val Asn Asn Ala Lys
165 170 175
Gly Ser Xaa Asn Leu Ser Ala Gly Gly Arg Thr Thr Ile Asn Asp Ala
180 185 190
Thr Ile Gln Ala Gly Ser Ser Val Tyr Ser Ser Thr Lys Gly Asp Thr
195 200 205

Xaa Leu Gly Glu Asn Thr Arg Ile Ile Ala Glu Asn Val Thr Val Leu
210 215 220
Ser Asn Gly Ser Ile Gly Ser Ala Ala Val Ile Glu Ala Lys Asp Thr
225 230 235 240
Ala His Ile Glu Ser Gly Lys Pro Leu Ser Leu Glu Thr Ser Thr Val
245 250 255
Ala Ser Asn Ile Arg Leu Asn Asn Gly Asn Ile Lys Gly Gly Lys Gln
260 265 270
Leu Ala Leu Leu Ala Asp Asp Asn Ile Thr Ala Lys Thr Thr Asn Leu
275 280 285
Asn Thr Pro Gly Asn Leu Tyr Val His Thr Gly Lys Asp Leu Asn Leu
290 295 300
Asn Val Asp Lys Asp Leu Ser Ala Ala Ser Ile His Leu Lys Ser Asp
305 310 315 320
Asn Ala Ala His Ile Thr Gly Thr Ser Lys Thr Leu Thr Ala Ser Lys
325 330 335
Asp Met Gly Val Glu Ala Gly Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
340 345 350
Xaa Xaa Xaa Ser Gly Asn Leu His Ile Gln Ala Ala Lys Gly Asn Ile
355 360 365
Gln Leu Arg Asn Thr Lys Leu Asn Ala Ala Lys Ala Leu Glu Thr Thr
370 375 380
Ala Leu Gln Gly Asn Ile Val Ser Asp Gly Leu His Ala Val Ser Ala
385 390 395 400

<210> 187
<211> 432
<212> PRT
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<220>
<223> Description of Artificial Sequence: homology

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<400> 187
 Leu Gln Gly Xaa Leu Gln Gly Lys Asn Xaa Xaa Xaa Xaa Xaa Gly Xaa
 1 5 10 15
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Gly Xaa Ile Xaa Ala Xaa Xaa Ala Xaa
 20 25 30

Xaa Xaa Lys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Ala Xaa Xaa Xaa Xaa
35 40 45
Xaa Xaa Xaa Ser Xaa Thr Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Val
50 55 60
Xaa Asn Xaa Gly Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Leu Xaa Xaa Xaa Xaa
65 70 75 80
Xaa Gly Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Ile Xaa Xaa Thr Ala
85 90 95
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Glu Xaa Thr Xaa
100 105 110
Xaa Xaa Xaa Xaa Gly Xaa Thr Xaa Xaa Xaa Xaa Xaa Gly Gly Xaa Ile Xaa
115 120 125
Ser Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Ile Xaa Xaa Xaa
130 135 140
Xaa Xaa Xaa Val Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Thr Xaa
145 150 155 160
Xaa Xaa Xaa Gly Xaa Asn Leu Xaa Xaa Xaa Xaa Xaa Lys Xaa Xaa Xaa Xaa
165 170 175
Xaa Xaa Xaa Xaa Xaa Val Xaa Xaa Xaa Xaa Xaa Gly Xaa Xaa Xaa Leu Xaa
180 185 190
Ala Gly Xaa Xaa Xaa Xaa Xaa Xaa Xaa Asp Xaa Xaa Xaa Xaa Ala Gly Xaa
195 200 205
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Tyr Xaa Xaa Xaa Xaa Gly
210 215 220
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Thr Arg Xaa Xaa Xaa Xaa Xaa Xaa Xaa
225 230 235 240
Xaa Xaa Xaa Xaa Gly Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Ile Xaa Xaa Xaa
245 250 255
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Gly Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
260 265 270
Thr Xaa Xaa Ser Xaa Xaa Xaa Xaa Asn Asn Xaa Xaa Xaa Lys Xaa Xaa
275 280 285
Xaa Xaa Xaa Xaa Xaa Xaa Ala Xaa Xaa Asn Xaa Xaa Xaa Lys Xaa Xaa
290 295 300
Xaa Xaa Xaa Xaa Xaa Gly Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Lys Asp
305 310 315 320
Xaa Xaa Xaa Asn Xaa Xaa Xaa Xaa Xaa Ser Xaa Xaa Xaa Xaa Xaa Xaa
325 330 335

Xaa Ser Xaa Asn Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa His Xaa Thr
340 345 350
Xaa Thr Xaa Xaa Thr Xaa Xaa Xaa Xaa Xaa Xaa Xaa Asp Xaa Gly Xaa Xaa
355 360 365
Xaa Gly Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
370 375 380
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Lys Gly Xaa Xaa Xaa Xaa Xaa Xaa Xaa
385 390 395 400
Xaa Xaa Xaa Asn Thr Xaa Xaa Xaa Ala Xaa Xaa Ala Xaa Xaa Xaa Xaa
405 410 415
Xaa Xaa Xaa Gly Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Ala Xaa Xaa Ala
420 425 430

<210> 188
<211> 402
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: pspA

<400> 188
Leu Gln Gly Asp Leu Gln Gly Lys Asn Ile Phe Ala Ala Ala Gly Ser
1 5 10 15
Asp Ile Thr Asn Thr Gly Ser Ile Gly Ala Glu Asn Ala Leu Leu Leu
20 25 30
Lys Ala Ser Asn Asn Ile Glu Ser Arg Ser Glu Thr Arg Ser Asn Gln
35 40 45
Asn Glu Gln Gly Ser Val Arg Asn Ile Gly Arg Val Ala Gly Ile Tyr
50 55 60
Leu Thr Gly Arg Gln Asn Gly Ser Val Leu Leu Asp Ala Gly Asn Asn
65 70 75 80
Ile Val Leu Thr Ala Ser Glu Leu Thr Asn Gln Ser Glu Asp Gly Gln
85 90 95
Thr Val Leu Asn Ala Gly Gly Asp Ile Arg Ser Asp Thr Thr Gly Ile
100 105 110
Ser Arg Asn Gln Asn Thr Ile Phe Asp Ser Asp Asn Tyr Val Ile Arg
115 120 125
Lys Glu Gln Asn Glu Val Gly Ser Thr Ile Arg Thr Arg Gly Asn Leu
130 135 140

Ser Leu Asn Ala Lys Gly Asp Ile Arg Ile Arg Ala Ala Glu Val Gly
 145 150 155 160
 Ser Glu Gln Gly Arg Leu Lys Leu Ala Ala Gly Arg Asp Ile Lys Val
 165 170 175
 Glu Ala Gly Lys Ala His Thr Glu Thr Glu Asp Ala Leu Lys Tyr Thr
 180 185 190
 Gly Arg Ser Gly Gly Gly Ile Lys Gln Lys Met Thr Arg His Leu Lys
 195 200 205
 Asn Gln Asn Gly Gln Ala Val Ser Gly Thr Leu Asp Gly Lys Glu Ile
 210 215 220
 Ile Leu Val Ser Gly Arg Asp Ile Thr Val Thr Gly Ser Asn Ile Ile
 225 230 235 240
 Ala Asp Asn His Thr Ile Leu Ser Ala Lys Asn Asn Ile Val Leu Lys
 245 250 255
 Ala Ala Glu Thr Arg Ser Arg Ser Ala Glu Met Asn Lys Lys Glu Lys
 260 265 270
 Ser Gly Leu Met Gly Ser Gly Gly Ile Gly Phe Thr Ala Gly Ser Lys
 275 280 285
 Lys Asp Thr Gln Thr Asn Arg Ser Glu Thr Val Ser His Thr Glu Ser
 290 295 300
 Val Val Gly Ser Leu Asn Gly Asn Thr Leu Ile Ser Ala Gly Lys His
 305 310 315 320
 Tyr Thr Gln Thr Gly Ser Thr Ile Ser Ser Pro Gln Gly Asp Val Gly
 325 330 335
 Ile Ser Ser Gly Lys Ile Ser Ile Asp Ala Ala Gln Asn Arg Tyr Ser
 340 345 350
 Gln Glu Ser Lys Gln Val Tyr Glu Gln Lys Gly Val Thr Val Ala Ile
 355 360 365
 Ser Val Pro Val Val Asn Thr Val Met Gly Ala Val Asp Ala Val Lys
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 Ala Val Gln Thr Val Gly Lys Ser Lys Asn Ser Arg Val Asn Ala Met
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 Ala Ala

<210> 189
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 <212> PRT
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 35 40 45
 Arg Tyr Thr Gly Asn Glu Tyr His Glu Ser Xaa Xaa Xaa Xaa Xaa Xaa
 50 55 60
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Asn Arg Lys Xaa Xaa Xaa
 65 70 75 80
 Xaa Xaa Xaa Arg Thr Asn Ile Val His Thr Gly Ser Ile Ile Gly Ser
 85 90 95
 Leu Asn Gly Asp Thr Val Thr Val Ala Gly Asn Arg Tyr Arg Gln Thr
 100 105 110
 Gly Ser Thr Val Ser Ser Pro Glu Gly Arg Asn Thr Val Thr Ala Lys
 115 120 125
 Xaa Ile Asp Val Glu Phe Ala Asn Asn Arg Tyr Ala Thr Asp Tyr Ala
 130 135 140
 His Thr Gln Glu Gln Lys Gly Leu Thr Val Ala Leu Asn Val Pro Xaa
 145 150 155 160
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Gly Lys
 165 170 175
 Ser Lys Asn Lys Arg Val Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Trp
 180 185 190
 Gln Ser Tyr Gln Ala Thr Gln Gln Met Gln Gln Phe Ala Pro Ser Ser
 195 200 205
 Ser Ala Gly Gln Gly Gln Asn Tyr Asn Gln Ser Pro Ser Ile Ser Val
 210 215 220
 Ser Ile Xaa Tyr Gly Glu Gln Lys Ser Arg Asn Glu Gln Lys Arg His
 225 230 235 240
 Tyr Thr Glu Ala Ala Ala Ser Gln Ile Ile Gly Lys Gly Gln Thr Thr
 245 250 255
 Leu Ala Ala Thr Gly Ser Gly Glu Gln Ser Asn Ile Asn Ile Thr Gly
 260 265 270
 Ser Asp Val Ile Gly His Ala Gly Thr Xaa Leu Ile Ala Asp Asn His
 275 280 285
 Ile Arg Leu Gln Ser Ala Lys Gln Asp Gly Ser Glu Gln Ser Lys Asn
 290 295 300
 Lys Ser Ser Gly Trp Asn Ala Gly Val Arg Xaa Lys Ile Gly Asn Gly
 305 310 315 320

Ile Arg Phe Gly Ile Thr Ala Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 325 330 335
 Xaa Xaa Xaa Ser Thr Thr His Arg His Thr His Val Gly Ser Thr Thr
 340 345 350
 Gly Lys Thr Thr Ile Arg Ser Gly Gly Asp Thr Thr Leu Lys Gly Val
 355 360 365
 Gln Leu Ile Gly Lys Gly Ile Gln Ala Asp Thr Arg Asn Leu His Ile
 370 375 380
 Glu Ser Val Gln Asp Thr Glu Thr Tyr Gln Ser Lys Gln Gln Asn Gly
 385 390 395 400
 Asn Val Gln Val Thr Val Gly Tyr Gly Phe Ser Ala Ser Gly Ser Tyr
 405 410 415
 Arg Gln Ser Lys Val Lys Ala Asp His Ala Ser Val Thr Gly Gln Ser
 420 425 430
 Gly Ile Tyr Ala Gly Glu Asp Gly Tyr Gln Ile Lys Val Arg Asp Asn
 435 440 445
 Thr Asp Leu Lys Gly Gly Ile Ile Thr Ser Ser Gln Ser Ala Glu Asp
 450 455 460
 Lys Gly Lys Asn Leu Phe Gln Thr Ala Thr Leu Thr Ala Ser Asp Ile
 465 470 475 480
 Gln Asn His Ser Arg Tyr Glu Gly Arg Ser Phe Gly Ile Gly Gly Ser
 485 490 495
 Phe

<210> 190
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 Gly Xaa Asp Ile Xaa Val Xaa Gly Xaa Xaa Xaa Ile Xaa Asp Xaa Xaa
 20 25 30
 Xaa Xaa Leu Xaa Ala Xaa Xaa Xaa Ile Xaa Xaa Xaa Xaa Ala Xaa Xaa
 35 40 45
 Arg Xaa Xaa Xaa Xaa Glu Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 50 55 60
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Lys Xaa Xaa Xaa
 65 70 75 80
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa His Thr Xaa Ser Xaa Xaa Gly Ser
 85 90 95
 Leu Asn Gly Xaa Thr Xaa Xaa Xaa Ala Gly Xaa Xaa Tyr Xaa Gln Thr
 100 105 110
 Gly Ser Thr Xaa Ser Ser Pro Xaa Gly Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 115 120 125
 Xaa Ile Xaa Xaa Xaa Xaa Ala Xaa Asn Arg Tyr Xaa Xaa Xaa Xaa Xaa

130						135						140					
Xaa	Xaa	Xaa	Glu	Gln	Lys	Gly	Xaa	Thr	Val	Ala	Xaa	Xaa	Val	Pro	Xaa		
145					150					155					160		
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa		
				165					170					175			
Xaa	Gly	Lys	Ser	Lys	Asn	Xaa	Arg	Val	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa		
			180					185						190			
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Ala	
		195					200					205					
Xaa	Xaa	Pro	Xaa	Xaa	Xaa	Ala	Gly	Gln	Gly	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa		
	210					215					220						
Xaa	Xaa	Ile	Ser	Val	Ser	Xaa	Xaa	Tyr	Gly	Glu	Gln	Lys	Xaa	Xaa	Xaa		
225					230					235						240	
Glu	Xaa	Xaa	Xaa	Xaa	Xaa	Thr	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Ile	Xaa	Gly		
				245					250					255			
Xaa	Gly	Xaa	Xaa	Xaa	Leu	Xaa	Ala	Xaa	Gly	Xaa	Gly	Xaa	Xaa	Ser	Xaa		
			260					265					270				
Ile	Xaa	Ile	Thr	Gly	Ser	Asp	Val	Xaa	Gly	Xaa	Xaa	Gly	Thr	Xaa	Leu		
	275						280					285					
Xaa	Ala	Xaa	Asn	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Ala	Xaa	Gln	Xaa	Xaa	Xaa		
	290					295						300					
Glu	Xaa	Ser	Xaa	Asn	Lys	Ser	Xaa	Gly	Xaa	Asn	Ala	Gly	Val	Xaa	Xaa		
305					310					315					320		
Xaa	Ile	Xaa	Xaa	Gly	Ile	Xaa	Phe	Gly	Xaa	Thr	Ala	Xaa	Xaa	Xaa	Xaa		
				325					330					335			
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Thr	Xaa	Xaa	Arg	Xaa	Xaa	His		
			340					345					350				
Xaa	Gly	Ser	Xaa	Xaa	Xaa	Xaa	Thr	Xaa	Ile	Xaa	Ser	Gly	Gly	Asp	Thr		
	355						360					365					
Xaa	Xaa	Lys	Gly	Xaa	Gln	Leu	Xaa	Gly	Lys	Gly	Xaa	Xaa	Xaa	Xaa	Xaa		
	370					375					380						
Xaa	Xaa	Leu	His	Ile	Glu	Ser	Xaa	Gln	Asp	Thr	Xaa	Xaa	Xaa	Xaa	Xaa		
385					390					395						400	
Lys	Gln	Xaa	Asn	Xaa	Xaa	Xaa	Gln	Val	Thr	Val	Gly	Tyr	Gly	Phe	Ser		
			405						410					415			
Xaa	Xaa	Gly	Ser	Tyr	Xaa	Xaa	Ser	Lys	Xaa	Xaa	Xaa	Asp	Xaa	Ala	Ser		
			420					425					430				
Val	Xaa	Xaa	Gln	Ser	Gly	Ile	Xaa	Ala	Gly	Xaa	Asp	Gly	Tyr	Xaa	Ile		
	435						440					445					

Xaa Val Xaa Xaa Xaa Thr Xaa Leu Xaa Gly Xaa Xaa Xaa Xaa Ser Xaa
 450 455 460
 Xaa Xaa Xaa Xaa Asp Lys Xaa Lys Asn Leu Xaa Xaa Thr Xaa Xaa Xaa
 465 470 475 480
 Xaa Xaa Xaa Asp Ile Gln Asn His Xaa Xaa Xaa Xaa Xaa Xaa Xaa
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<210> 191
 <211> 491
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<220>
 <223> Description of Artificial Sequence: pspA

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 Thr Ile Leu Ser Ala Lys Asn Asn Ile Val Leu Lys Ala Ala Glu Thr
 35 40 45
 Arg Ser Arg Ser Ala Glu Met Asn Lys Lys Glu Lys Ser Gly Leu Met
 50 55 60
 Gly Ser Gly Gly Ile Gly Phe Thr Ala Gly Ser Lys Lys Asp Thr Gln
 65 70 75 80
 Thr Asn Arg Ser Glu Thr Val Ser His Thr Glu Ser Val Val Gly Ser
 85 90 95
 Leu Asn Gly Asn Thr Leu Ile Ser Ala Gly Lys His Tyr Thr Gln Thr
 100 105 110
 Gly Ser Thr Ile Ser Ser Pro Gln Gly Asp Val Gly Ile Ser Ser Gly
 115 120 125
 Lys Ile Ser Ile Asp Ala Ala Gln Asn Arg Tyr Ser Gln Glu Ser Lys
 130 135 140
 Gln Val Tyr Glu Gln Lys Gly Val Thr Val Ala Ile Ser Val Pro Val
 145 150 155 160
 Val Asn Thr Val Met Gly Ala Val Asp Ala Val Lys Ala Val Gln Thr
 165 170 175
 Val Gly Lys Ser Lys Asn Ser Arg Val Asn Ala Met Ala Ala Ala Asn

180										185					190				
Ala	Leu	Asn	Lys	Gly	Val	Asp	Ser	Gly	Val	Ala	Leu	Tyr	Asn	Ala	Ala				
		195						200					205						
Arg	Asn	Pro	Lys	Lys	Ala	Ala	Gly	Gln	Gly	Ile	Ser	Val	Ser	Val	Thr				
	210					215					220								
Tyr	Gly	Glu	Gln	Lys	Asn	Thr	Ser	Glu	Ser	Arg	Ile	Lys	Gly	Thr	Gln				
225					230					235					240				
Val	Gln	Glu	Gly	Lys	Ile	Thr	Gly	Gly	Gly	Lys	Val	Ser	Leu	Thr	Ala				
				245					250					255					
Ser	Gly	Ala	Gly	Lys	Asp	Ser	Arg	Ile	Thr	Ile	Thr	Gly	Ser	Asp	Val				
			260					265					270						
Tyr	Gly	Gly	Lys	Gly	Thr	Arg	Leu	Lys	Ala	Glu	Asn	Ala	Val	Gln	Ile				
	275						280					285							
Glu	Ala	Ala	Arg	Gln	Thr	His	Gln	Glu	Arg	Ser	Glu	Asn	Lys	Ser	Ala				
	290					295					300								
Gly	Phe	Asn	Ala	Gly	Val	Ala	Ile	Ala	Ile	Asn	Lys	Gly	Ile	Ser	Phe				
305					310					315					320				
Gly	Phe	Thr	Ala	Gly	Ala	Asn	Tyr	Gly	Lys	Gly	Tyr	Gly	Asn	Gly	Asp				
				325					330					335					
Glu	Thr	Ala	Tyr	Arg	Asn	Ser	His	Ile	Gly	Ser	Lys	Asp	Ser	Gln	Thr				
			340					345					350						
Ala	Ile	Glu	Ser	Gly	Gly	Asp	Thr	Val	Ile	Lys	Gly	Gly	Gln	Leu	Lys				
	355						360					365							
Gly	Lys	Gly	Val	Gly	Val	Thr	Ala	Glu	Ser	Leu	His	Ile	Glu	Ser	Leu				
	370					375					380								
Gln	Asp	Thr	Ala	Val	Phe	Lys	Gly	Lys	Gln	Glu	Asn	Val	Ser	Ala	Gln				
385					390					395					400				
Val	Thr	Val	Gly	Tyr	Gly	Phe	Ser	Val	Gly	Gly	Ser	Tyr	Asn	Arg	Ser				
			405						410					415					
Lys	Ser	Ser	Ser	Asp	Tyr	Ala	Ser	Val	Asn	Glu	Gln	Ser	Gly	Ile	Phe				
			420					425					430						
Ala	Gly	Gly	Asp	Gly	Tyr	Arg	Ile	Arg	Val	Asn	Gly	Lys	Thr	Gly	Leu				
	435						440					445							
Val	Gly	Ala	Ala	Val	Val	Ser	Asp	Ala	Asp	Lys	Ser	Lys	Asn	Leu	Leu				
	450					455					460								
Lys	Thr	Ser	Glu	Ile	Trp	His	Lys	Asp	Ile	Gln	Asn	His	Ala	Ser	Ala				
465					470					475					480				
Ala	Ala	Ser	Ala	Leu	Gly	Leu	Ser	Gly	Gly	Phe									

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<220>
 <223> Description of Artificial Sequence: ORF41

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 Xaa Gln Leu Gln Val Thr Lys Asp Val Asn Trp Asn Gln Val Xaa Leu
 35 40 45
 Ala Tyr Asp Lys Trp Asp Tyr Lys Gln Glu Gly Leu Thr Gly Ala Gly
 50 55 60
 Ala Ala Ile Ile Ala Leu Ala Val Thr Val Val Thr Ala Gly Ala Gly
 65 70 75 80
 Ala Gly Ala Ala Leu Gly Leu Asn Gly Ala Ala Ala Ala Ala Thr Asp
 85 90 95
 Ala Ala Phe Ala Ser Leu Ala Ser Gln Ala Ser Val Ser Leu Ile Asn
 100 105 110
 Asn Lys Gly Asn Ile Gly Asn Thr Leu Lys Glu Leu Gly Arg Ser Ser
 115 120 125
 Thr Val Lys Asn Leu Met Val Ala Val Ala Thr Ala Gly Val Ala Asp
 130 135 140
 Lys Ile Gly Ala Ser Ala Leu Asn Asn Val Ser Asp Lys Gln Trp Ile
 145 150 155 160

Asn Asn Leu Thr Val Asn Leu Ala Asn Ala Gly Ser Ala Ala Leu Ile
 165 170 175
 Asn Thr Ala Val Asn Gly Gly Ser Leu Lys Asp Asn Leu Glu Ala Asn
 180 185 190
 Ile Leu Ala Ala Leu Val Asn Thr Ala His Gly Glu Ala Ala Ser Lys
 195 200 205
 Ile Lys Gln Leu Asp Gln His Tyr Ile Thr His Lys Ile Ala His Ala
 210 215 220
 Ile Ala Gly Cys Ala Ala Ala Ala Asn Lys Gly Lys Cys Gln Asp
 225 230 235 240
 Gly Ala Ile Gly Ala Ala Val Gly Glu Ile Val Gly Glu Ala Leu Thr
 245 250 255
 Asn Gly Lys Asn Pro Asp Thr Leu Thr Ala Lys Glu Arg Glu Gln Ile
 260 265 270
 Leu Ala Tyr Ser Lys Leu Val Ala Gly Thr Val Ser Gly Val Val Gly
 275 280 285
 Gly Asp Val Asn Ala Ala Ala Asn Ala Ala Glu Val Ala Val Lys Asn
 290 295 300
 Asn Gln Leu Ser Asp Lys
 305 310

<210> 193
 <211> 330
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: ORF41a

<220>
 <221> SITE
 <222> (61)
 <223> place-holder

<220>
 <221> SITE
 <222> (122)
 <223> place-holder

<220>
 <221> SITE
 <222> (158)
 <223> place-holder

<220>
 <221> SITE
 <222> (280)

<223> place-holder

<220>

<221> SITE

<222> (297)

<223> place-holder

<400> 193

Tyr Leu Lys Gln Leu Gln Val Ala Lys Asn Ile Asn Trp Asn Gln Val
1 5 10 15

Gln Leu Ala Tyr Asp Arg Trp Asp Tyr Lys Gln Glu Gly Leu Thr Glu
20 25 30

Ala Gly Ala Ala Ile Ile Ala Leu Ala Val Thr Val Val Thr Ser Gly
35 40 45

Ala Gly Thr Gly Ala Val Leu Gly Leu Asn Gly Ala Xaa Ala Ala Ala
50 55 60

Thr Asp Ala Ala Phe Ala Ser Leu Ala Ser Gln Ala Ser Val Ser Phe
65 70 75 80

Ile Asn Asn Lys Gly Asp Val Gly Lys Thr Leu Lys Glu Leu Gly Arg
85 90 95

Ser Ser Thr Val Lys Asn Leu Val Val Ala Ala Ala Thr Ala Gly Val
100 105 110

Ala Asp Lys Ile Gly Ala Ser Ala Leu Xaa Asn Val Ser Asp Lys Gln
115 120 125

Trp Ile Asn Asn Leu Thr Val Asn Leu Ala Asn Ala Gly Ser Ala Ala
130 135 140

Leu Ile Asn Thr Ala Val Asn Gly Gly Ser Leu Lys Asp Xaa Leu Glu
145 150 155 160

Ala Asn Ile Leu Ala Ala Leu Val Asn Thr Ala His Gly Glu Ala Ala
165 170 175

Ser Lys Ile Lys Gln Leu Asp Gln His Tyr Ile Val His Lys Ile Ala
180 185 190

His Ala Ile Ala Gly Cys Ala Ala Ala Ala Asn Lys Gly Lys Cys
195 200 205

Gln Asp Gly Ala Ile Gly Ala Ala Val Gly Glu Ile Val Gly Glu Ala
210 215 220

Leu Thr Asn Gly Lys Asn Pro Asp Thr Leu Thr Ala Lys Glu Arg Glu
225 230 235 240

Gln Ile Leu Ala Tyr Ser Lys Leu Val Ala Gly Thr Val Ser Gly Val
245 250 255

Val Gly Gly Asp Val Asn Ala Ala Ala Asn Ala Ala Glu Val Ala Val

	260		265		270										
Lys	Asn	Asn	Gln	Leu	Ser	Asp	Xaa	Glu	Gly	Arg	Glu	Phe	Asp	Asn	Glu
	275						280					285			
Met	Thr	Ala	Cys	Ala	Lys	Gln	Asn	Xaa	Pro	Gln	Leu	Cys	Arg	Lys	Asn
	290					295					300				
Thr	Val	Lys	Lys	Tyr	Gln	Asn	Val	Ala	Asp	Lys	Arg	Leu	Ala	Ala	Ser
305					310					315					320
Ile	Ala	Ile	Cys	Thr	Asp	Ile	Ser	Arg	Ser						
				325					330						

<210> 194
 <211> 180
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: ORF51a

<400> 194

Tyr	Lys	Leu	Leu	Ala	Ile	Gly	Ser	Val	Val	Gly	Ser	Ile	Leu	Gly	Val
1				5					10					15	
Lys	Leu	Leu	Leu	Ile	Leu	Pro	Val	Ser	Trp	Leu	Leu	Leu	Leu	Met	Ala
			20					25					30		
Ile	Ile	Thr	Leu	Tyr	Tyr	Ser	Val	Asn	Gly	Ile	Leu	Asn	Val	Cys	Ala
		35				40						45			
Lys	Ala	Lys	Asn	Ile	Gln	Val	Val	Ala	Asn	Asn	Lys	Asn	Met	Val	Leu
	50				55						60				
Phe	Gly	Phe	Leu	Ala	Gly	Ile	Ile	Gly	Gly	Ser	Thr	Asn	Ala	Met	Ser
65					70					75				80	
Pro	Ile	Leu	Leu	Ile	Phe	Leu	Leu	Ser	Glu	Thr	Glu	Asn	Lys	Asn	Arg
				85					90					95	
Ile	Ala	Lys	Ser	Ser	Asn	Leu	Cys	Tyr	Leu	Leu	Ala	Lys	Ile	Val	Gln
			100					105					110		
Ile	Tyr	Met	Leu	Arg	Asp	Gln	Tyr	Trp	Leu	Leu	Asn	Lys	Ser	Glu	Tyr
	115						120					125			
Gly	Leu	Ile	Phe	Leu	Leu	Ser	Val	Leu	Ser	Val	Ile	Gly	Leu	Tyr	Val
	130					135					140				
Gly	Ile	Arg	Leu	Arg	Thr	Lys	Ile	Ser	Pro	Asn	Phe	Phe	Lys	Met	Leu
145					150					155					160
Ile	Phe	Ile	Val	Leu	Leu	Val	Leu	Ala	Leu	Lys	Ile	Gly	Tyr	Ser	Gly
				165				170						175	

Leu Ile Lys Leu
180

<210> 195

<211> 180

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: ORF82a

<400> 195

Met Arg His Met Lys Asn Lys Asn Tyr Leu Leu Val Phe Ile Val Leu
1 5 10 15

His Ile Thr Leu Ile Val Ile Asn Ile Val Phe Gly Tyr Phe Val Phe
20 25 30

Leu Phe Asp Phe Phe Ala Phe Leu Phe Phe Ala Asn Val Phe Leu Ala
35 40 45

Val Asn Leu Leu Phe Leu Glu Lys Asn Ile Lys Asn Lys Leu Leu Phe
50 55 60

Leu Leu Pro Ile Ser Ile Ile Ile Trp Met Val Ile His Ile Ser Met
65 70 75 80

Ile Asn Ile Lys Phe Tyr Lys Phe Glu His Gln Ile Lys Glu Gln Asn
85 90 95

Ile Ser Ser Ile Thr Gly Val Ile Lys Pro His Asp Ser Tyr Asn Tyr
100 105 110

Val Tyr Asp Ser Asn Gly Tyr Ala Lys Leu Lys Asp Asn His Arg Tyr
115 120 125

Gly Arg Val Ile Arg Glu Thr Pro Tyr Ile Asp Val Val Ala Ser Asp
130 135 140

Val Lys Asn Lys Ser Ile Arg Leu Ser Leu Val Cys Gly Ile His Ser
145 150 155 160

Tyr Ala Pro Cys Ala Asn Phe Ile Lys Phe Ala Lys Lys Pro Val Lys
165 170 175

Ile Tyr Phe Tyr
180